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Copyright (c) 1993 - 2003 Compugen Ltd.
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	PD	-MAY-	1997.					
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	PA PA	(AJIN) (KIKU/)	AJINO	TINOMOTO CO I	INC.			
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	X X	da Y,		Jima T;				
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide used to design a probe to screen for gastric cancer antigen gene.
                                                                                                             This novel peptide is a fragment of a gastric cancer antigen present in a human gastric cancer cell, which when bound to a human leukocyte antigen (HLA), is capable of inducing a cytotoxic I lymphocyte (CTL) response that targets the gastric cancer cell. A second peptide (AAW16577) has also been produced, containing amino acids 1-9 of the present sequence. However, peptides containing amino acids 1-9 of the present sequence have no CTL inductivility, and cannot be used. HLA-bound peptides can be used to treat or prevent gastric cancer. Wirses, e.g. waccinia virus, or bacteria, e.g. BCG, which contain the DNA encoding this peptide can be used as a live vaccine for preventing or treating human gastric cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antigen proteins, useful for the prevention and treatment of human
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                cell
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            Gastric cancer antigen fragment present in human gastric cancer - induces cytotoxic I lymphocyte response when bound to human leukocyte antigen, for gastric cancer treatment or prevention
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                                                                                Claim 3; Page 9; 14pp; English.
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The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and CPP associated with an antigen for a disease, by providing (I) and (2) preparing a composition for a disease, and introducing the antigen-associated CPP to (I), where antigen enters into the cell. The antigens are, for example, tumour antigen enters into the cell. The antigens dby tumour infilitrating lymphocytes (TIL) of HLA (human lenconfied by tumour infilitrating lymphocytes (TIL) of HLA (human lenconfied by tumour infilitrating lymphocytes (TIL) of HLA (human lenconfied by tumour disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal, such that following the administration, animal is protected from disease, where the animal comprises both CD4 and CD8 T cells. It is also useful to treating a disease (e.g. cancer, tumour, melanoma, thymoma, clung cancer, non-Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,
                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
cytotoxic I cell response. The gastric cancer antigen polynucleotide can be used in a recombinant virus or bacterium as a vaccine. The gastric cancer antigen polypeptides are also used for the prevention or treatment of human gastric cancer.
                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
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                                                                                                                                        Length 10;
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                                                                                                                                                                                                                                                                                                                                                            ABG79110 standard; Peptide; 10 AA.
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kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (I), preferably dendritic cell is prior to, subsequent to or concurrent with, the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This novel peptide is a fragment of a gastric cancer antigen present in a human gastric cancer cell, which when bound to a human leukocyte antigen (HLA), is capable of inducing a cytotoxia. I lymphocyte (CTL) response that targets the gastric cancer cell. It is based on amino acids 1-9 of peptide 1 (AAM16576), whih shows the same effect. However, peptides containing amino acids 1-8 and 1-7 of peptide 1 have no CTL inducibility, and cannot be used. The HLA-bound peptides can be used to treat or prevent gastric cancer. Viruses, e.g. vaccinia virus, or basteria, e.g. BCG, which contain the DNA encoding this peptide can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                live vaccine for preventing or treating human gastric cancer.
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gastric cancer, gastric cancer antigen; human leukocyte antigen;
HLA; cytotoxic I lymphocyte; CTL; recombinant bacterium;
recombinant virus; gastric cancer; vaccine.
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The present immunodeficiency virus-1 (HTV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HTV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, or particularly when compared to the use of whole antiqens in vaccines. Compositions. There is evidence that the immune response to whole antiqens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in a lowing for immune escape due to mutations. The groups for inclusion in a lowing for immune escape due to mutations the likelihood of callowing for immune escape due to mutations. The groups that may be present in whole antigens can be selected from conserved regions of viral or the composition of the groups (CTL and HTL) and further, to modify the composition advantage of an group-based vaccines.

An additional advantage of an group-based vaccine approach is the ability to composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. Appl1501 to ABP25412
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                                                                                                                                                                                                                                                                                                            HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Livingston BD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S, Livin
Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                           HIV A24 super motif env peptide #63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 32; Page 180; 448pp; English.
                                                                                                                                                             ABP15183 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000; 2000WO-US27766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0412863.
                                                                                                                                                                                                                                        (first entry)
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Celis E,
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                                  1 YSWMDISCW
                                                                   1 YSWMDISCW
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Matches 4; Conserv
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Baker DM,
                                                                                                                                                                                                  ABP15183;
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                                                                                                                         RESULT 5
                                                                                                                                              ABP15183
                                  δλ
                                                                     a
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Length 9;

Score 61; DB 18; Pred. No. 9.3e+05;

100.0%;

93.88;

Query Match Best Local Similarity

HIV A24 super motif env peptide #172.

(first entry)

.5-JUL-2002

ABP15292;

ABP15292 standard; Peptide; 9 AA.

RESULT 7 ABP15292

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escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity, Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP22412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
                                                                                                                                                                                                                                                                                              vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                           HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chesnut R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide groups, useful for vaccinating against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 32; Page 362; 448pp; English.
                                                                                                                    ABP24036 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                    HIV A24 motif env peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000; 2000WO-US27766.
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                                                                                                                                                                                                (first entry)
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Celis E,
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| ||: |:
1 WFDITNWL
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Baker DM,
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                                                                          RESULT 6
                                                                                                   ABP24036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL2534) to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}\textsc{-}1
                                                                                                          HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Pred. No. 9.3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Livingston BD,
                                                                                                                                                                                                                                                                                                                                                                                                               S, Livin
Grey HM;
                                                                                                                                                                                   Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kubo RT,
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Celis E,
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Baker DM,
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Matches
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RESULT 8 ABP15394

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Gaps

0;

Length 8;

49.2%; Score 32; DB 22; Length 8; 50.0%; Pred. No. 9.3e+05; ive 2; Mismatches 2; Indels

4; Conservative

Local Similarity

Best Loc Matches

Query Match

3 WMDISCWI 10

δy qq

WFDITNWL 8

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RESULT 10
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                                                                                              HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Pred. No. 9.3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                               Southwood S, Livingston BD,
Kubo RT, Grey HM;
                                                                        HIV A24 super motif env peptide #274.
                                                                                                                                              Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 32; Page 184; 448pp; English.
 ABP15394 standard; Peptide; 9 AA.
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50.0%;
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                                                                                                                                                                                                                      05-OCT-2000; 2000WO-US27766.
                                                 (first entry)
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                                                                                                                                                                                                                                                                                              Sidney J,
, Celis E,
                                                                                                                                                                                                                                                                      (EPIM-) EPIMMUNE INC
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Best Local Similarity
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                                                                                                                                                                      WO200124810-A1.
                                                                                                                                                                                                                                              05-OCT-1999;
                                                 15-JUL-2002
                                                                                                                                                                                               12-APR-2001
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                        ABP15394;
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ID ABP1
XX
AC ABP1
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QΣ
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
                                                                                                                       HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Pred. No. 9.3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide groups, useful for vaccinating against HIV-1
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                                                             HIV A24 super motif env peptide #365.
                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
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Kubo RT,
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(first entry)
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Celis E,
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15-JUL-2002
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Baker DM,
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12-APR-2001
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Baker DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP55412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                  compositions comprising human immunodeficiency virus-1 (HIV-1) groups, useful for vaccinating against {\rm HIV}\textsc{-}1
                                   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
vpu; vif; tat; cytotoxic I lymphocyte; CTL; immune response; epitope;
antigen; vaccine; HIV infection; immunisation; virucide.
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                                                                                                                                                                                                                                                                                                                                          Livingston BD,
                                                                                                                                                                                                                                                                                                                             Southwood S, Livir
                                                                                                              Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 32; Page 273; 448pp; English.
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HIV A01 motif env peptide #8.
                                                                                                                                                                                                                           05-OCT-2000; 2000WO-US27766.
                                                                                                                                                                                                                                                                99US-0412863
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine compositions
                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                        Sette A, Sidney J,
Baker DM, Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WFDITNWL 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                   WO200124810-A1.
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ABP19896
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human immunodeficiency virus—1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (BAL534) to ABP5397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the
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vpu; vif; tat; cytotoxic I lymphocyte; CIL; immune response; epitope;
antigen; vaccine; HIV infection; immunisation; virucide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide groups, useful for vaccinating against HIV-1
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Kubo RT, Grey HM;
                                                                                                                        Human immunodeficiency virus type 1.
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Celis E,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (cTL and HTL), and further, to modify the immunogenicity, Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP25412
                                                                                                                                                                                                   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}{-1}
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                                                                                                                                              Chesnut R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 22; Length 9;
Pred. No. 9.3e+05;
2; Mismatches 2; Indels
                                                                                                                                            Livingston BD,
                                                                                                                                           S, Livir
Grey HM;
Human immunodeficiency virus type 1.
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                                                                                                                                          Southwood
Kubo RT,
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50.0%;
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                                                                    05-OCT-2000; 2000WO-US27766.
                                                                                           99US-0412863
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                   (EPIM-) EPIMMUNE INC.
                                                                                                                                         Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 WMDISCWI 10
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                                                                                           05-OCT-1999;
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Baker DM,
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the present interition describes a composition of 1 composition and a prepared human immunodeficiency virus-1 (HTV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABR25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunishing subjects against HTV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, compositions. There is evidence that the immune response to whole artigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in a group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of the word of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, and further, to modify the form of form the form of the groups, and further, to modify the form of form of forms.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}\textsc{-}1
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                                                                                                                                                                                                                                                                       Southwood S, Livingston BD, Chesnut R;
Kubo RT, Grey HM;
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50.0%;
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Celis E,
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                   05-0CT-1999;
12-APR-2001
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                                                                                                                                                                                                                                                                   Sette A,
Baker DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nvention
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completed: August 4, 2003, 12:15:16
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06-JUL-1999;
             07-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                          syndromes
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Job time :
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                                                                                                                                                                                                                                                                                                                                                                                                   escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (ZTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPLISG1 to ABP22412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                               particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                              human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines,
                                                                                                                                                                                                                                present invention describes a composition (1) comprising a prepared
                                                                                                                                                           Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phage display; antianaemic; cytostatic; immunosuppressive; immunoglobulin M; IgM; IgM binding; autoimmune haemolytic anaemia; paraneoplastic syndrome; multiple myeloma; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                      Chesnut R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 22; Length 9;
Pred. No. 9.3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                          peptide groups, useful for vaccinating against HIV-1
                                                                                   S, Livingston BD, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phage clone ed1 pIII-displayed peptide.
                                                                                                                                                                                                     Claim 32; Page 362; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB66551 standard; peptide; 9 AA.
                                                                                      Southwood
                                                                                                     Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.2%;
 05-OCT-2000; 2000WO-US27766.
                              99US-0412863.
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                                                         (EPIM-) EPIMMUNE INC
                                                                                    Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||: |:
WFDITNWL 8
                                                                                                                                WPI; 2001-354887/37
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Baker DM,
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The present sequence is one of a number of random 9-mer peptides which were displayed from the N-terminal portion of the pIII capsid protein of filamentous bacteriophage MI3XBSI. Peptides that selectively bind to inmunoglobulin (19)M antibodies but do not selectively bind to immunoglobulin (19)M antibodies but do not selectively bind to antibodies of other classes were identified. Such peptides are useful for detecting the peptides are also useful for isolating an antigen specific IgM population. They are useful for treating a human disease associated with population. They are useful for treating a human disease associated with isohaemagglutinin binding to red blood cells, autoimmune haemolytic anaemia, paraneoplastic syndromes, multiple myeloma or cancer. The peptides are useful for treating diseases such as cancer or an autoimmune disease associated with IgM antibodies by removing IgM from serum. The peptides are capable of selectively binding to the IgM molecules of several mammalian species and to both the pentameric and
                                                                                                                                                                                                                                                                                                                      Novel peptides that bind to immunoglobulin M antibodies and block their interaction with antigens, useful for treating rheumatoid factor biding to immunoglobulin G, autoimmune hemolytic anemia or paraneoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                  Cutler JE;
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99US-0142389
                                  99US-0142524
                                                                                                            (RERE-) RES & DEV INST INC.
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                                                                                                                                                                                  Glee PM, Pincus SH,
                                                                                                                                                                                                                                                        WPI; 2001-138063/14
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Best Local Similarity
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                                                                       (without alignments)
14.590 Million cell updates/sec
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Sequence 44,
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Sequence 3,
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Sequence 9,
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                                                         August 4, 2003, 12:13:55; Search time 29 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-082-279B-1480
US-09-315-304B-1634
US-09-431-539-11
US-08-431-539-11
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US-08-862-855-13
US-09-226-985-13
US-09-227-906-13
US-09-311-784A-222
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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US-08-178-570-69
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PCT-US95-00147-69
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US-08-723-116-2
US-09-103-808-2
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US-09-103-808-3
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                                                                                                                                                                       328717 seqs, 42310858 residues
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                                       - protein search, using sw model
                                                                                                                                                                                                                                                                  Listing first 45 summaries
                                                                                                                                                   Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                         Maximum Match 100%
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65
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Match Length DB
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                                                                                                                       Sequence:
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                                                         Run on:
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No.
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Sequence 6, Appli Sequence 16, Appl Sequence 39, Appl	16, 39, 55, 64,	Sequence 64, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 18, Appl	Sequence 23, Appl Sequence 18, Appl Sequence 18, Appl Sequence 62, Appl Sequence 4, Appli Sequence 28, Appli
US-08-559-492-6 US-09-059-111-16 US-09-059-111-39	PCT-US95-08353-16 PCT-US95-08353-39 US-08-271-830-55 US-09-258-754-64	US-US-U4Z-1U/-64 US-08-159-339A-469 US-09-059-111-24 PCT-US95-08353-24 US-08-190-788A-18	US-08-383-474B-23 US-08-465-391A-18 US-08-464-538B-18 US-08-463-076E-62 US-08-907-403A-4 US-08-757-316C-28
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ALIGNMENTS

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PEPTIDE CAPABLE OF INDUCING IMMUNE
RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-821-0X
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-723-116-1
; Sequence 1, Application US/08723116
Patent No. 5837248
; GENERAL INFORMATION:
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TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                         SAHARA, HIROMITSU
                                                                                                                                                                                                                                                                                                                                                       WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
                                                                                                                                                                                  KIKUCHI, KOKICHI
SATO, NORIYUKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                     APPLICANT: TABOJIMA, TANA APPLICANT: TABOJIMA, TANA APPLICANT: WADA, YOSHIMA PPLICANT: SULVIX, WANA APPLICANT: HAMURO, JUNJITLE OF INVENTION: PEPTITLE OF INVENTION: OR'ITLE OF INVENTION: OR'INVENTION: OR'INVENTIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 2
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USA
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PEPTIDE CAPABLE OF INDUCING IMMUNE
RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                        Gaps
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KIKUCHI, KOXichi
APPLICANT: SATO, No. 64448001yuki
APPLICANT: SAHARA, Hiroeki
APPLICANT: TORIGOE, TOShihiko
APPLICANT: SGUKI, Manabu
APPLICANT: SUZUKI, Manabu
APPLICANT: HAMURO, Junji
TITLE OF INVENTION: Human Gastric Cancer Antigen Gene and Gastric
TITLE OF INVENTION: Cancer Antigen Protein
FILLE REFERENCE: 09871
CURRENT APPLICATION NUMBER: US/09/348,265
CURRENT FILING DATE: 1999-07-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
Length 10;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.C.
1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
100.0%; Score 65; DB 4; ]
100.0%; Pred. No. 0.00031;
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: JP 10-197852
EARLIER FILLING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SAHARA, HIROMITSU
APPLICANT: YASOIMA, TARAHIRO
APPLICANT: WADA, YOSHIMASA
APPLICANT: WADA, YOSHIMASA
APPLICANT: HAWURO, JUNNI
TITLE OF INVENTION: PEPTIDE CAPA
TITLE OF INVENTION: RESPONSE TO
TITLE OF INVENTION: OR TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-723-116-2; Sequence 2, Application US/08723116; Patent No. 5837248
                                                                                                                                                                                                                             Sequence 3, Application US/09348265 Patent No. 6444800
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APPLICANT: KIKUCHI, KOKICHI
APPLICANT: SATO, NORIYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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                                                                                   1 YSWMDISCWI 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-348-265-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                             1 YSWMDISCWI
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      Query Match
Best Local Similarity
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ADDRESSEE:
                                             10;
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                                                                                                                                                                                        RESULT 3
US-09-348-265-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
LENGTH: 10
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                                             Matches
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                                                                                                                                                                                             0;
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADE,
                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
                                                                                                                                                  100.0%; Score 65; DB 2; Length 10; 100.0%; Pred. No. 0.00031; Eive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUTCATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/723,116
FILING DATE: CURKOWND-
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/103,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09103808 Patent No. 6368852 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIKUCHI, KOKICHI
SATO, NORIYUKI
SAHARA, HIROMITSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUZUKI, MANABU
HAMURO, JUNJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22202
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                           Best Local Similarity 100.
Matches 10; Conservative
                           TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                              1 YSWMDISCWI 10
                                                                                                                                                                                                                                       1 YSWMDISCWI 10
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                                                                                          ; ORGANISM: HUMAN US-08-723-116-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-103-808-1
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                                                                                                                                                          Query Match
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GENERAL INFORMATION:
APPLICANT: KINCCHI, KOKICHI
APPLICANT: SATO, NORITUKI
APPLICANT: SAHRA, HIROMITSU
APPLICANT: SAHRA, HIROMITSU
APPLICANT: YASOJIMA, TAKAHIRO
APPLICANT: WADA, YOSHIMASA
APPLICANT: WADA, YOSHIMASA
APPLICANT: WADA, YOSHIMASA
APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
NUMBER OF SEQUENCES: 4
ADDRESS:
ADDRESS:
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STREET: 175 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.8%; Score 61; DB 4; Length 9; 100.0%; Pred. No. 2.5e+05; ative 0; Mismatches 0; Indels
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SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/723,116
FILING DATE: 30-SEP-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-SEP-1995
                                                                                  NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET WUMBER: 10-821-0X
TELECOMMONICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEPHAX: 703-413-220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                  APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/08723116
Patent No. 5837248
                                                                                                                                                                                                                                                                   LENGIH: 9 amino acids
                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPRY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YSWMDISCW 9
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US-08-723-116-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.8%; Score 61; DB 2; Length 9; 100.0%; Pred. No. 2.5e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,808
FILING DATE: 24-Jun-1998
CLASSIFICATION: <URKNOWN>
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: JP 217140/1996
FILING DATE: JP-MG-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
RESERRENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,116
                       APPLICATION NUMBER: US/08/723,116
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SATO, NORIYUKI
SAHARA, HIROMITSU
YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09103808
Patent No. 6368852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KIKUCHI, KOKICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HAMURO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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Best Local Similarity
Matches 9; Conserv
                                            FILING DATE: 30 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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δă qq 10-821-0X

REFERENCE/DOCKET NUMBER:

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TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                  Gaps
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                                                                                                                                          76.9%; Score 50; DB 4; Length 8; 100.0%; Pred. No. 2.5e+05; Live 0; Mismatches 0; Indels
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FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: DP 253491/1995
FILING DATE: 29-SEP-1995
PRIOR APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
                 MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08723116
Patent No. 5837248
GENERAL INFORMATION:
APPLICANT: KIRUCHI, KOKICHI
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REFERENCE/DOCKET NUMBER: 10-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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APPLICANT: WADA, YOSHIMASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SATO, NORIYUKI
APPLICANT: SAHARA, HIROMITSU
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HAMURO, JUNJI
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TOPOLOGY: linear
                                                                                                                                               Query Match 76.9
Best Local Similarity 100.
Matches 8; Conservative
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US-08-723-116-4
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ADDRESSEE:
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APPLICANT:
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US-08-723-116-4
                                                                                                       US-09-103-808-3
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STATE:
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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                                                                                                                                                                                                                                                                                                76.9%; Score 50; DB 2; Length 8; 100.0%; Pred. No. 2.5e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERAIING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMER: US/09/103,808
FLIGHG DATE: 24-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/723,116
FILING DATE: -CURKNOWN-
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10-821-0X TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
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TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09103808
Patent No. 6368852
GENERAL INFORMATION
APPLICANT: KIKUCHI, KOKICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SATO, NORIYUKI
SAHARA, HIROMITSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER:
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           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                    INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
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                          : 703-413-3000
703-413-2220
                                                                                                                                                                                                                                                                                                       Query Match 76.9
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                            LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
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                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                TOPOLOGY:
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                                                    TELEFAX:
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Query Match

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Gaps
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                                                                                                                                                 APPLICANT: Buchardt, Ole
APPLICANT: Breddam, Klaus
APPLICANT: Breddam, Klaus
APPLICANT: Henriksen, Dennis
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: C-Terminally Amidated Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anwer, Mohmed
APPLICANT: Lambert, Dennis
IITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,539
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,306
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/082,279B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1515
                                                                                                                                                                                                                                                                    STREET: Mineapolis
STATE: Mineapolis
STATE: Mineapolis
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                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         Sequence 9, Application US/08431539
Patent No. 5580751
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
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US-08-431-539-9
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Best Local Similarity
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1 YGWMDFA 7
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ZIP: 55402
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                                                                        US-08-431-539-9
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APPLICANT:
APPLICANT:
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RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,808
FILING DATE: 24-Jun-1998
CLASSIFICATION: CURROWN>
Score 41, DB 2, Length 7;
Pred. No. 2.5e+05;
0; Mismatches 0; Indels
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APPLICATION NUMBER: 08/723,116
FILING DATE: CORKNOWN>
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 4: US-09-103-808-4
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WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
                                                                                                                                                                                                                Sequence 4, Application US/09103808
Patent No. 6368852
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 SATO, NORIYUKI
SAHARA, HIROMITSU
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  63.1%; s
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                   7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Best Local Similarity 100.0
Matches 7; Conservative
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              Best_Local Similarity
Matches 7; Conserv
                                                                           1 YSWMDIS 7
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1 YSWMDIS 7
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                                                                   3: Indels
                               Length 8;
                                                                                                                                                                                                                                  Sequence 11, Application US/08431539
Patent No. 5580751
GENERAL INFORMATION.
GENERAL INFORMATION.
FOR THE BUCHART. BUCHART, Ole
APPLICANT: Buchardt, Ole
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: C-Terminally Amidated Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE: 10
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5580751west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29; DB 1;
Pred. No. 2.5e+05;
0; Mismatches 1
                               Score 30; DB 4; 1
Pred. No. 2.5e+05;
1; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,306
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08431539
Patent No. 5580751
GENERAL INFORMATION:
APPLICANT: Buchardt, ole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.6%;
80.0%;
                                    46.2%;
50.0%;
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Breddam, Klaus
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                   Query Match
Best Local Similarity 50...
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Matches 4; Conservative
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US-09-834-784-1480
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US-08-431-539-15
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APPLICANT: Merutka, G.
APPLICANT: Merutka, G.
APPLICANT: Anwer, M.
APPLICANT: Lambert, D.
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
TITLE OF INVENTION: PROPERTIES
FILE REPERENCE: 7872-052
CURRENT APPLICATION NUMBER: US/09/315,304B
CURRENT FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
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                                                                                                                                 Score 30; DB 3; Length 8; 
Pred. No. 2.5e+05; 
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barney, Shawn
APPLICANT: Guthrie, Kelly
APPLICANT: Guthrie, Kelly
APPLICANT: Merutka, Gene
APPLICANT: Amwer, Mohmed
APPLICANT: Lambert, Dennis
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
TITLE OF INVENTION: HARMACOKINETIC PROPERTIES
FILE REFERENCE: 7872-043
CURRENT APPLICATION NUMBER: US/09/834,784
CURRENT FILING DATE: 2001-04-13
CURRENT FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 1515
SOFTWARE: FastSEQ for Windows Version 3.0
         FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 1667
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1634
                                                                                                                                                                                                                                                                                                                                       Sequence 1634, Application US/09315304B Patent No. 6348568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1480, Application US/09834784 Patent No. 6562787
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Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                           Best Local Similarity 50.0
Matches 4; Conservative
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US-09-315-304B-1634
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LENGIH: 8
                                                                                   ORGANISM: SIV
                         SEQ ID NO 1480
LENGIH: 8
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                                                                   TYPE: PRT
             SOFTWARE:
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APPLICANT: Henriksen, Dennis
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: C-perminally Amidated Peptides
COMPRESENE: Morchart & Could
STREET: 3100 No. 5580751west Center
STATE: Mineapolis
COMPITY: Mineapolis
STATE: Mineapolis
STATE: Mineapolis
COMPITY: Mineapolis
COMPITY: Mineapolis
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COMPITY: Mineapolis
COMPITY: His Process
COMPITY
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Search completed: August 4, 2003, 12:18:47 Job time : 29 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 4, 2003, 12:12:50 ; Search time 38 Seconds (without alignments) 25.308 Million cell updates/sec

US-09-103-808-1 65 1 YSWMDISCWI 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

1100 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	neuromodulatory pe			н	obolemetelisis	Obologiatoriating	chologratokinin =	lengelyscokinin .	rbwllogaewilet	phytrocaerulein -	caelulein Irog (cderulein-like pep	peptide-N4-(N-acet	19 neavy chain CRD	נטטו	1		Q,				₩.	⊣ .	cytochrome-c oxida	Š		CVTOChTOMO-C OWIGE	
SUMMARIES	QI	333244	32	33	ும	T027	A32516	P00012	43001	JS0318	A61357	A61337	A13687	A59272	DT0322	AKTOTM	Phonos	D 57444	701367	A21114	717054	T17063	B57444	PT0245	T14215	T14223	B34835	_	10	12303
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	Score	27	27	25	23	23	22	. 22	22	22	22	22	22	22	22	21.5	21	20	20	20	20	20	19	19	19	19	18	18	18	18
	Result No.	П	5	e	4	2	9	7	ထ	o	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	29

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717060 712308 717072 712316 712316 712323 73223 809552 809552 809552 112376 712323 7114043
попринивирини
100 110 100 100 100 100 100 100 100
22222222222222222222222222222222222222
18 18 18 18 17 17 17 17 17 17 17 17
8888888888844444 CHQ848667890HQ849

ALIGNMENTS

ganglia c	0;
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RESULT 1 S33.244 neutromodulatory peptide WMamide-1 - giant African snail C;Species: Achatina fulica (giant African snail) C;Species: Achatina fulica (giant African snail) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997 C;Accession: S33.244 EEBS Lett. 323, 104-108, 1993 A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia c A;Reference number: S33.244; MUID:93265912; PMID:8495720 A;Reference number: A;Retatus: preliminary A;Accession: S33.244 A;Residues: 1-7 <min></min>	; Length 7; 05; 2; Indels
RESULT 1 S33.24 neuromodulatory peptide Wwamide-1 - giant African snail C;Species: Achatina fullica (giant African snail) C;Dete: 19-war-1997 #sequence_revision 19-war-1997 #text C;Accession: S33.244 EEBS Lett. 323, 104-108, 1993 A;Reference number: S33.244; MUID:93265912; PMID:8495720 A;Reference number: S33.244 A;Accession: S33.244 A;Residues: 1-7 <min></min>	Ouery Match 41.5%; Score 27; DB 2; Length 7; Best Local Similarity 42.9%; Pred. No. 2.8e+05; Matches 3; Conservative 2; Mismatches 2; Indels 3 WMDISCW 9
wwamide-1 - Lica (giant Alica (giant Alaquence_revis: T.; Muneoka, J. 1993 and -3: novel and -3: nov	41.5%; Sc 42.9%; Pr vative 2;
RESULT 1 S33.24 C.Species: Achatina full. C.Species: Achatina full. C.Species: Achatina full. C.Sacession: S33.24 ERMINERATA, H.; Ikeda, T. FEBS Lett. 3.23, 104-108, A.Title: Wammide-1, -2 at A.Reference number: S33.24 A.Reference number: S32.44 A.Referession: S33.24 A.Reference number: A.Reference number	tch al Similarity 42.9 3; Conservative 3 WMDISCW 9 :: 1 WKEMSVW 7
RESULT 1 S3324 neuromodulatory pept (Species: Achaina C;Date: 19-Mar-1997 C;Accession: S33244 R.Minakata, H.; Iked FEBS Lett. 323, 104-A;Title: WWannde-1, A;Reference number: A;Reference number: A;Accession: S33244 A;Status: preliminar A;Molecule type: pro A;Residues: 1-7 <min< td=""><td>Ouery Mat Best Locs Matches Oy</td></min<>	Ouery Mat Best Locs Matches Oy

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	of caps				1000	/66T-TDO- 5 7	ن
<pre> ; Length 7; 05; 2: Indels</pre>	לי דוומעדמ			snail	# ++ 02+ 03+ 12 04 04 04 04 04 04 04 04 04 04 04 04 04	* ceat_change	M.; Nomoto, F
<pre>; Score 27; DB 2; ; Pred. No. 2.8e+0 2: Mismatches</pre>				giant African	frican snail)	100 mm - 100 mm	i.; Kobayashi,
ar ar		:: } KEMSVW 7		S33245 neuromodulatory peptide WWamide-2 - giant African snail	C;Species: Achatina fulica (giant African snail) C;Date: 19-Mar-1997 #sequence regision 19-Mar-1907 #+524 phage 20 723 1902	ode H . Windowski	FEBS Lett. 323, 104-108, 1993
Query Match Best Local Similarity 42.9 Matches 3; Conservative	3 WMDISCW 9	1 WKEMSVW 7	RESULT 2	245 comodulatory per	becies: Achatina te: 19-Mar-1997	C; Accession: S33245 R: Minakata H : Ivod	FEBS Lett, 323, 104-108, 1993
Z À Z	δŏ	qq	RES	S33245 neuromo	C; S]	C; A	FEB

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A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33245
A;Accession: S33245
A;Actuar: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>
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42.9%; Pred. No. 2.8e+05;
ive 2; Mismatches 2; Indels
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Best Local Similarity 42.9
Matches 3; Conservative
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RESULT 3 S33246 neuromodulatory peptide WWamide-3 - giant African snail C;Species: Achatina fulica (giant African snail)

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0;

Gaps

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0; Indels Length

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C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
B;Shively, J; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCR-5: Sequence analysis of a small cholecystokinin from canine brain and in A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 1-5 <SH1>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 22; DB 2; Lv 100.0%; Pred. No. 2.8e+05; tive 0; Mismatches 0;
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Best Local Similarity 100.v
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C'Speciés: Alo-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C'Accession: Pr0272
R'Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R'Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A'Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: Pr0222; MUID:91108337; PMID:1899102
                                                                                                                        A;ritle: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of A;Reference number: S33244; MUID:93265912; PMID:8495720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Species: Gryllus binaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
B;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J; Biol. Chem. 270, 21103-21108, 1995
A;Teference number: A57444; MUID:95403341; PMID:7673141
A;Accession: C57444
A;Accession: C57444
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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                         C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
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                                                                            R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, FEBS Lett. 323, 104-108, 1993
                                                                                                                                                                                                                                                                                                   Score 25; DB 2; Length 7; Pred. No. 2.8e+05; limitatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 2; Length 9;
Pred. No. 2.8e+05;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuropeptide Grb-AST B3 - two-spotted cricket
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Accession: PT0272
A,Molecule type: DNA
A,Residues: 1-9 <YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                        38.5%;
42.9%;
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50.0%;
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Best Local Similarity 60.0°
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Best Local Similarity 50.00
Matches 3; Conservative
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                                                                                                                                                                                                       A Status: preliminary
A Molecule type: protein
A Residues: 1-7 <MIN>
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nes 3; Conserv
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1 WKQMSVW 7
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                                                          C; Accession: S33246
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C;Species: Macropus eugenii (tammar wallaby)
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 30-oct-1992 #sequence_revision 30-oct-1992 #text_change 13-Sep-1996
C;Accession: A43001; P20012
A;Fith: C:Moolecystokinin octapeptide purified from brains of Australian marsuplals.
A;Reference number: P20012; MUID:88234141; PMID:3375140
A;Reference number: A33001
C.Species: Dasyurus viverrinus (southeastern quoll)
C.Becies: Dasyurus viverrinus (southeastern quoll)
C.Becession: P00012
C.Becession: P00012
Peptides 9, 429-431, 1988
A.Title: Cholecystckinin octapeptide purified from brains of Australian marsupials.
A.Reference number: P00012; MUID:88234141; PMID:3375140
A.Reference number: P00012
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C; Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F; 2/Finding site: sulfate (Tyr) (covalent) #status predicted
F; 8/Modified site: amidated carboxyl end (Phe) #status predicted
                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted
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A, Molecule type: protein
A, Rolecule type: protein
A, Residues: 1-10 < ANA>
A, Residues: 1-10 < ANA>
C, Comment: The last five amino acids and the carboxyl terminal amide group of this n. C, Comment: This amphibian skin peptide can cause a sustained lowering of blood press C, Superfamily: gastrin
C, Keywords: amidated carboxyl end; antihypertensive, neuropeptide; pyroglutamic acid F, L/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental
F, L/Modified site: sulfate (Tyr) (covalent) *status experimental
F, L/Modified site: amidated carboxyl end (Phe) *status experimental
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R. Monteucchi, P.; Falconieri Erspamer, G.; Visser, J.

A. Title: Occurrence of Asn(13), Leu(5), Caerulein in the skin of the African frog Hylamk A. Reference number: A13687; MUID:77246547; PMID:891852

A. Reference number: A13687; MUID:77246547; PMID:891852

A. Accession: A13687

A. Monteule type: protein

A. Fesidues: 1-10 CMON>
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C; Species: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C; Accession: A59272
F; Altanan, F; Paschinger, K; Dalik, T; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A; Title: Characterisation of peptide-Nat/N-accetyl-beta-glucosaminyl) asparagine amidas
A; Reference number: A59272; MUID:98181894; PMID:9523720
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C;Species: Kassina maculata
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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(S. Superfamily: gastrin
(S. Superfamily: gastrin
(S. Superfamily: gastrin
(S. F. I. Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
(F. I. Modified site: sulfate (Tyr) (covalent) #status experimental
(F. I. Modified site: anidated carboxyl end (Phe) #status experimental
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Pred. No. 8.6e+02;
1; Mismatches 1;
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100.0%; Pred. No. 8.6e+02;
Live 0; Mismatches 0;
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60.0%;
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A:Molecule type: protein
A:Residues: 1-10 <ALT>
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Best Local Similarity
Matches 3; Conserv
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C; Keywords: hydrolase
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R; Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A; Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin A; Reference number: J50317
A; Reference number: J50318
A; Accession: J50318
A; Access
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A)Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nons A; Reference number: A61357; MUID:70005484; PMID:5824931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sulfoprotein
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                                                                                                                                                                                                                                                                                                 leucokinin VIII - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Phyllomedusa sauvagei (Saŭvage's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Hyla caerulea
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
                 Gaps
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C; Superfamily: gastrin
C; Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin;
F;1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental
F;3/Binding site: sulfate (Tyr) (covalent) *status experimental
F;9/Modified site: amidated carboxyl end (Phe) *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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C; Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate C; Keywords: amidated carboxyl end: cephalomyotropic peptide F:8/Modified site: amidated carboxyl end (Gly) #status experimental
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                 Indels
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Arch. Bloochem. Bloophys. 125, 57-68, 1968
A; Title: Isolation and amino acid sequence of caerulein,
A; Reference number: A61337; MUID:68238534; PMID:5649531
A; Accession: A61337
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A;Status: preliminary
A;Molecule type: protein
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C) Species: Locusta migratory locust C) Species: Locusta migratoria (migratory locust C) Species: Locusta migratoria (migratory locust) C) Date: 31 Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998 C; Accession: A60065 R; Accession: A60065 R. Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A. Regul. Pept. 36, 111-119, 1991 A; Particle: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI A) Reference number: A60065; MUID:92179466; PMID:1796179
                              A; Molecule type: protein
A; Residues: 1-9 <SCH>
C; Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and
C; Superfamily: locustamyoinhibiting peptide
C; Superfamily: locustamyoinhibiting peptide
C; Keywords: amidated carboxyl end; hormone
F; 9/Modified site: amidated carboxyl end (Trp) #status experimental
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 4, 2003, 12:06:05; Search time 24 Seconds (without alignments) 19.594 Million cell updates/sec Run on:

US-09-103-808-1 65 1 YSWMDISCWI 10

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

372 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 10

Post-processing: Minimum Match 0%
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Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
Bombycidae; Bombyx.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Sigmurethra; Achatinoidea; Achatinidae; Achatina.
NCBL_TaxID=6530;
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"Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from gangline of the African giant snail, Achatina fulica.";
FEBS Lett. 323:104-108(1993).
PIR: S33246; S33346.
Nouropeptide, Amidation.
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MEDLINE-20002634; PubMed=10531308;
Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
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                     MOD_RES 7 7 AMIDATION.
SEQUENCE 7 AA, 965 MW; 7362D5B69B132310 CRC64;
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28-FBB-2003 (Rel. 41, Last annotation update)
20-thoracicostatic peptide (Bom-PTSP).

Bombyx mori (Silk moth).
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MEDLINE=93265912; PubMed=8495720;
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Kataoka H.;
J. Biol. Chem. 275:9892-9892(2000).
J. Biol. Chem. Inhibits ecdysteroid biosynthesis in the prothoracic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macropus eugenii (Tammar Wallaby), and
Dasyurus viverzinus (Southeastern quoll).
Bukaryota: Metacoca; Chordatta; Craniata; Vertebrata; Euteleostomi;
Mammalia: Metatheria; Diprotodontia; Macropodidae; Macropus.
NCBL_TaxID=9315, 9279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                     ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- STMILARTY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A43001; A43001.
PIR; PQ0012; PQ0012.
InterPro; IPR001551; Gastrin.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Sulfation; Hormone.
MOD_RES
                                                                                                                                                                                                                                                37.7%; Score 24.5; DB 1; Length 9; 44.4%; Pred. No. 1.3e+05; ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 22; DB 1; Length 8; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 1064 MW; DDCAA68378768B5A CRC64;
                                                                                                                                                                                                      3878C5B4472AB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucckinin VIII (L-VIII).
Leuccophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Cholecystokinin (CCK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA.
                                                                               gland.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Preq. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION
                                                                                                                                                                              AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=M.eugenii, and D.viverrinus;
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88234141; PubMed=3375140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.8%;
                                                                                                                                                                                                   SEQUENCE 9 AA; 1090 MW;
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us-09-103-808-1.lim10.rsp

Mon Aug

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Amidation; Neuropeptide.
                                                                                                                                                                                                                                                                                                                               Query Match 33.1
Best Local Similarity 33.3
Matches 3; Conservative
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                          σ
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                                                                                                                                                                                                                                                                               PIR; A60065; AKLQIM
                                                                                                                                                                                                                                                                                                                                                                          2 SWMDISC-W
                                     LMIP_LOCMI P31799;
                                                                                                                                                                                                                                                  OVIDUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GON3_ONCKE
                                                                                                                                                               SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE.
                                                                                                                                                                                                                                                                                                  MOD_RES
                           LMIP_LOCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                        GON3_ONCKE
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                 RESULT 8
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                                      셤
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                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                     Australian tree frog Litoria xanthomera.";

J. Pept. Sci. 3:1811-185(1997).

J. Pept. Sci. 3:1811-185(1997).

J. SUBCELLULAR LOCATION: Secreted.

J. SUBCELLULAR LOCATION: Secreted.

J. TISSUE SPECIFFCITY: Skin dorsal glands.

J. MASS SPECTROMETRY: MW-1354; METHOD-FAB.

J. SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

InterPro; IPR001651; Gastrin.

PROSITE: PS00259; GASTRIN; 1.

Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;

Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
Eukaryota; Metazoa; Arthropoda; Hexapoda; insecta; rellyyoua;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
Blaberidae; Leucophaea.
                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                            Score 22; DB 1; Length 8; Pred. No. 1.3e+05; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33.8%; Score 22; DB 1; Length 10; 100.0%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99DBF3837861BB5A CRC64;
                                                                                                                                                                              AMIDATION.
736365AB59CAADD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                             10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                      Litoria xanthomera (Orange-thighed frog).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMIDATION
                                                                                                                                                                                                   33.8%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Skin secretion;
MEDLINE=97374000; PubMed=9230483;
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SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AA; 1290 MW;
                                                                                                                                                                                        8 AA; 902 MW;
                                                                                                                                                       PIR; JS0318; JS0318.
Neuropeptide; Amidation.
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=79697;
                                                                                                                                                                                                                                                                 |||
5 YSW 7
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                                                                                                                                                                                                                                                   1 YSW 3
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                                                              TISSUE=Head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MMD
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                                                                                                                                                                                                                                                                                                                           CAER_LITXA
                                                                                                                                                                                                                                                                                                                                                                               Caerulein.
                                                                                                                                                                                     SEQUENCE
                                                    SEQUENCE
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Best Local 9
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                                                                                                                                                                          MOD_RES
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p20367; P81751; Created)
01-FEB-1991 (Rel. 17, Created)
01-FEB-1993 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
                                                                                                                                                                                                                                                                                                                                        egul. Pept. 36:111-119(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBOESOPHAGEAL GANGLION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3
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Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes; Salmonidae, Oncorhynchus.
NCBI_TaxID=8018, 30724;
                                                                                                                                                                                                                                                            Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; "Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria."

Regul. Pept. 36:111-119(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE.
SPECIES-0. teta;
MDDLINE-83195140; PubMed-6341999;
Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale 'Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale 'Characterization of a teleost gonadotropin-releasing hormone.";
"Characterization of a teleost gonadotropin-releasing hormone.";
"Characterization of Sci. U.S.A. 80:2794-2798(1983).
                              01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 27, Last annotation update)
01-ocustamyoinhibiting peptide (LOM-MIP).
Locustamyoinhibiting peptide (LOM-MIP).
Eukaryota: Metazoa: Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera: Orthopteroidaa; Orthoptera; Caelifera; Acridioner, Acridione, Acridione, Locusta.
NCBI_TAXID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 21.5; DB 1; Length 9;
Pred. No. 1.3e+05;
3; Mismatches 2; Indels
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9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus keta (Chum salmon), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clupea pallasii (Pacific herring).
                                                                                                                                                                                                                                            MEDLINE=92179466; PubMed=1796179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.1%;
33.3%;
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Query Match
Best Local Similarity
                                                                                                                                                                                                   1 YSW 3
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         IISSUE=Head;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                P82086;
                                                                                                                                                                                                                                                   RESULT 12
CA12_LITCI
                                                                                                                                                                                 Matches
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0;
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0
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                                                                                                                                              Gaps
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-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILLE
-1- SUNLYARITY: OF COCKROACH PROYDDEUM (HINGUT).
-1- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                  01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
1-MAY-1991 (Rel. 18, Last annotation update)
1-Geocokinin IV (L-IV).
1-Geocophae maderae (Madeira cockroach).
1-Geocophae maderae (Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leucokinin VI (L-VI).
Leucophaea maderae (Madeira cockroach).
Eukaryota: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
                                                                                                                                              0
secretion of both luteinizing and follicle-stimulating
                                                                          Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid. MOD_RES
                                                                                                                        Score 20; DB 1; Length 10;
Pred. No. 8.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                        284B3233786B45A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.2%; Score 17; DB 1; 1
66.7%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                          -i- SIMILARITY: Belongs to the GNRH family. PIR; A21114; A21114. InterPro; IPR02012; GNRH.
                                                                                              AMIDATION
                    SUBCELLULAR LOCATION: Secreted
                                                                                                                          30.8%;
50.0%;
                                                                                                        10 AA; 1230 MW;
                                                        Pfam; PF00446; GnRH; 1.
PROSITE; PS00473; GNRH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide; Amidation.
MOD_RES 8 8
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                                                                                                                                     Best_Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                       Blaberidae; Leucophaea.
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                    Cephalomyotropins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6988
                                                                                              10
                                                                                                                                                                1 YSWM 4
                                                                                                                                                                                  5 YGWL 8
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P19988;
                                                                                                                                                                                                                                  LCK4_LEUMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOD_RES
SEQUENCE
                                                                                              MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                             Query Match
                                                                                                                                                                                                                                            P21143;
                                                                                                                                                                                                                RESULT 10
LCK4_LEUMA
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LCK6_LEUMA
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MEDLINE-87052651; PubMed-2877794;
Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure, and synthesis of leucokinins V and VI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wabbitz P.A., Bowie J.H., Tyler M.J.; "Caerulein-like peptides from the skin glands of the Australian blue montains tree frog Litoria citropa. Part 1. Sequence determination
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sulfated.
--- MASS SPECTROMETRY: MW-1366; METHOD-Electrospray.
--- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
InterPro: IPR001651; Gastrin.
PROSITE; PS00259; GASTRIN; FALSE_NEG.
Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
                                                             myotropic peptides of Leucophaea maderae.";

Comp. Biochem. Physiol. 88C:27-30(1987).

-1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-1- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND PIR; JS0316; JS0316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Litoria citropa (Australian blue mountains tree frog), and Litoria splendida (Magnificent tree frog). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                         Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
MOD_RES 8 AMIDATION.
SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 FDF64
                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 1; Length 8;
Pred. No. 1.3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using electrospray mass spectrometry.";
Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Caerulein 1.2/1.2x4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=L.citropa; TISSUE=Skin secretion; MEDLINE=20057701; PubMed=10589099;
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                                                                                                                                                                                                                                                                                                                                                                                        26.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pelodryadinae, Litoria.
NCBI_TaxID=94770, 30345;
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-!-FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                        TISSUE-Skin secretion, Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Corellidae; Chelyosoma.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
NCBI_TaxID=104895;
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
                        Score 17; DB 1; Length 10;
Pred. No. 2.5e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
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 99DBFCD37861BB5A CRC64;

        MOD_RES
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        6
        AMIDATION.

        SEQUENCE
        6
        AA; 792 MW; 6683704772C9A000 CRC64;

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28-FEB-2003 (Rel. 41, Last sequence update)
15-SFP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                     Aust. J. Chem. 52:639-645(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                     Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                        26.28;
66.78;
 1306 MW;
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                                 Best Local Similarity
Matches 2; Conserv
 10 AA;
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Matches 2; Conserv
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P80677;
SEQUENCE
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                        Query Match
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Moilusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
NCBL_TaxID=89766;
                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides 21:623.630(2000).
-!- FUNCTION: Cardioactive; has both positive chronotropic and inotropic effects on the heart. Ocp-4 is a 1000 time less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                      Score 16; DB 1; Length 10;
Pred. No. 3.6e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.1%; Score 15; DB 1; Length 4; 100.0%; Pred. No. 1.3e+05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active than Ocp-3.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
26-FEB-2003 (Rel. 41, Last annotation update)
Octopus minor (Octopus).
                                                                                                                                                                                                                                                                                                                                                                                                                            4 AA.
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                                                                                                                                                                                                                      24.68;
66.78;
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Best Local Similarity 100.v.

Hest 2; Conservative
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TISSUE=Brain;
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SEQUENCE
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August 4, 2003, 12:12:30; Search time 93 Seconds (without alignments) 27.748 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                     OM protein - protein search, using sw model
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sp_human:*
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sp_archeap:* sp_vertebrate:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_virus:* SPTREMBL_23:* Database :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

099213 aegilops sq P81899 prunus dulc 09pru9 sparus aura 035835 rattus sp. Q15888 homo sapien Q9try3 sus sp. ins Q9try3 sus sp. ins Q9t819 liolaemus a Q9t84 liolaemus r Q9t87 liolaemus m Q9t87 liolaemus m Q9t87 hoplocercus Q7988 basiliscus Q7988 basiliscus Q7988 eublepharus Q9t87 eublepharus Q9try5 eublepharus Description SUMMARIES Q99213 P81899 Q9PRU9 O35885 Q15888 Q9TRY3 Q9TRP3 Q9TRP9 Q9TRP0 Q9TRP0 Q9TRP0 Q9TRP0 Q9TRP0 079888 Q9T8P0 Q9TFV5 Q9T4Y2 079897 Query Match Length DB 333.8 330.8 330.8 330.8 330.8 330.8 330.8 Score 120 120 130 130 130 130 130 130 Result N N

01-MAR-2001 (TrEMBLrel. 16, Created) 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large

10 AA.

PRT;

PRELIMINARY;

P81899; P81899

P81899 ID P8 AC P8 DT 01 DT 01 DE DE

RESULT 2

Q89131 borrelia bu Q89126 borrelia bu Q16386 homo sapien Q9483 diploglossu Q8siu4 xantusia sri Q94201 heloderma s Q8sit8 xantusia ar Q94544 anguis frag Q94544 anguis frag Q94544 anguis frag Q94574 xantusia vi Q94577 sauresia ag P92774 xantusia vi Q8siu1 xantusia vi Q8siu1 zantusia vi Q8siu1 zantusia vi Q94871 liolaemus m Q94811 liolaemus m Q94813 liolaemus c Q94847 phymaturus Q94847 phymaturus Q94848 liolaemus c Q94841 liolaemus c	tte) phyta; Tracheophyta; es; Poaceae; Pooideae; illo C., asarda D.D.; CRC64; Length 10; i; Indels 0; Gaps 0;
9 2 QBGL31 9 2 QBGL26 10 8 Q9TGB3 10 8 Q9TGB1 10 8 Q9TGA1 10 8 Q9TGA1 10 8 Q9TGA4 10 8 Q9TGA4 10 8 Q9TGA4 10 8 Q9TGA7 10 8 Q9TGA7 10 8 Q9TBY7 10 8 Q9TBY6 10 8 Q9	PRT; 10 AA. Created) Last sequence upde Last annotation upde Created Last annotation upde Created Cre
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TISSUE-Testis;
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"Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A and its N-glycans.":
Eur. J. Biochem. 252:118-123(1998).
-!- CATALYNIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-GLUCOSAMINYL)ASPRAGINE RESIDDE IN WHICH THE N-ACETYL-D-GLUCOSAMINE RESIDDE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-glycosidase) (N-glycanase) (Fragment).
Prunus dilcis (Almond) (Prunus amyqdalus).
Eukaryota, Viridiplantae; Ereptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Powell J.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.;
"Three forms of gonadotropin-releasing hormone characterized from brains of one species.";

Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).

SEQUENCE 10 AA; 1132 MW; 81566865AB587735 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sparus aurata (Gilthead sea bream).
Bukaryota, Metazoa, Chordata, Caniata, Vertebrata, Euteleostomi, Actinopteryoli, Neopteryoli, Teleostei, Euteleostei, Neoteleostei, Acanthomorpha, Acanthopteryoli, Percomorpha, Perciformes, Percoidei,
                                                                                                                                                                                                      SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE CONTAINING AN ASPARTIC RESIDUE.
SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
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DEGLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.8%; Score 22; DB 13; Length 10; 100.0%; Pred. No. 2.4e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                            Length 10;
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Pred. No. 2.4e+03;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Gonadotropin-releasing hormone, SBGNRH-I.
                                                                                                                                                                                                                                                                    -! - MASS SPECTROMETRY: MW=54182; METHOD=MALDI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA.
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                                                                                                  AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                       10 AA; 1106 MW;
                                                                                                                                                                                                                                                                                                                              33.8%;
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NON_TER 10 10
SEQUENCE 10 AA; 1106 M
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Best Local Similarity
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6 HSWAD 10
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NCBI_TaxID=8175;
                                                                         NCBI_TaxID=3755;
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                                                                                                              PubMed=9523720;
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                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
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                                                                                                                                                                                                                                                                               MEDLINE-98008057; PubMed-9581555; Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.; Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.; Human and rat testis express two mRNA species encoding varients of NRD convertase, a metalloendopeptidase of the insulinase family."; EMBL; X93208; CAA63695.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Homo sapiens (Human).
Eukaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum: Mol. Genet. 0:0-0(1995).
EMBL; L32069; AAA73878.1; -.
NON_TER 8 8 8
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
05, Created)
05, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                886 MW; EA7EA1B1ADC5A5B6 CRC64;
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  01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Best Local Similarity
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                                          MEDLINE-92049376; PubMed-1719383; Shimasaki S., Gao L., Shimasaki S., Ling N.; Ing N.; Indation and molecular cloning of insulin-like growth factor-binding protein-6.";
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Lepidosauria; Squamata; Iguania; Iguanidae; Iropidurinae; Liolaemus.
NCBI_TaxID=109394;
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Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
NCBI_TaxID=109412;
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                                                                                                                                          30.8%; Score 20; DB 6; Length 8; 100.0%; Pred. No. 8.3e+05; ative 0; Mismatches 0; Indels
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                    8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;
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            NCBI_TaxID=9826
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Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.; "Philogenetic relationships in the iguanid lizard Genus Liolaemus: Multiple origins of viviparous reproduction and evidence for recurring Andean vicariance and dispersal.", Biol. J. Linn. Soc. 69:75-102(2000). EMBL: AF099253; AAF18865.1; -. Mitochondrion.
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STRAIN-SDSU3498;
Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
Phylogenetic relationships in the ignanid lizard Genus Liolaemus:
Multiple origins of vivipacrous reproduction and evidence for recurring Andean vicariance and dispersal.";
Biol. J. Linn. Soc. 69:75-102(2000).
EMBL; AF099220; AAF18766.1; -.
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Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus,
NCBI_TaxID=109435;
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Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
NCBI_TaxID=166936;
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2: Mismatches 2; Indels
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Pred. No. 5.1e+03;
2; Mismatches 2; Indels
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SEQUENCE 10 AA; 1254 MW; 1A3580C733640440 CRC64;
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01-MAY-2000 (TLEMBLrel. 13, Last sequence update)
01-DEC-2001 (TEMBLrel. 19, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
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01-MAR-2002 (TIEMBLEEL. 20, Last sequence update)
01-MAR-2002 (TIEMBLEEL. 20, Last annotation update)
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42.9%;
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42.9%;
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Best Local Similarity 42.9
Matches 3; Conservative
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SEQUENCE
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mitochondrial genome among iguanian lizards.";
J. Mol. Evol. 44:660-674(1997).
EMBL; U82683; AAC62284.1; -.
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                                                 EMBL; vor.
Mitochondrion.
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Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
Multiple origins of viviparous reproduction and evidence for recurring
Andean vicariance and dispersal.";
Biol. J. Linn. Soc. 69:75-102(2000).
EMBL: AF099247; AAF18847.1;
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Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
NCBI_TaxID=109468;
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Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
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Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
"Evolutionary shifts in three major structural features of the
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Pred. No. 5.1e+03;
Pred. 2; Indels
                                                                                                                                                                       Score 20; DB 8; Length 10; Pred. No. 5.1e+03;
                                                                                                                                                                                                                  2; Indels
          montanus, Liolaemus molinai.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF305915; AAL55815.1; --
EMBL, AF305916; AAL55818.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AA; 1254 MW; 1A3580C733640440 CRC64;
                                                                                                             NON_TER 10 10 10
SEQUENCE 10 AA; 1254 MW; 1A3580C733640440 CRC64;
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42.9%;
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                                                                                                                                                                         30.8%;
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nes 3; Conserv
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Best Local Similarity
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Matches
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Q9T8N7
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Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Iguania; Iguanidae; Corytophaninae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=97315309; PubMed=9169559;

MACHINE=97315309; P.A., Ananjeva N.B., Papenfuss T.J.;

MACHINES J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;

"Evolutionary shifts in three major structural features of the mitochondrial genome among iguanian lizards.";

J. Mol. Evol. 44.660-674(1997).

EMBL, U82680; AAC62269.1;
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                                              Length 10;
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0A3480C7336415B0 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
Cytochrome o oxidase subunit I (Fragment).
                             Score 20; DB 8; Ler
Pred. No. 5.1e+03;
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                                              a 30.8%;
Similarity 57.1%;
4; Conservative
       10 AA; 1288 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Basiliscus plumifrons.
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Best Local Similarity
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                                                                    Best Local Similarity
Matches 4; Conserv
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NON_TER 10
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Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
"Vicariant patterns of fragmentation among gekkonid lizards of the
phylogenetic perspective and an area cladogram for central asia.";
Mol. Phylogenet. Evol. 12:320-332(1999).
Mitochondrion.

NON_TER

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10

SEQUENCE 10 AA; 1241 MW; 5DEE80C7336415B7 CRC64;
                                                                                                                                                                                                                                                                                                                                              Mitochondrion.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Gekkota; Eublepharidae;
Eublepharus.

NCBI_TaxID=52219;
                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                    Score 20; DB 8; Length 10;
Pred. No. 5.1e+03;
2: Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 8; Length 10;
Pred. No. 5.1e+03;
2; Mismatches 2; Indels
                                            1A3580C733640440 CRC64;
                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
Cytochrome c oxidase subunit I (Fragment).
                                                                                                                                                                                                                                    10 AA
                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                   PRT;
                                                                       30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.8%;
42.9%;
EMBL; AF099246; AAF18844.1;
Mitochondrion.
                          NON_TER 10 10
SEQUENCE 10 AA; 1254 MW;
                                                                   Query Match
Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
                                                                                                                                                                                                                                                                                                                                  Eublepharus turkmenicus.
                                                                                                                              4 MDISCWI 10
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Best Local Similarity
Matches 3; Conserv
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Q9TFV5
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Search completed: August 4, 2003, 12:17:28 Job time : 96 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 4, 2003, 12:20:21; Search time 39 Seconds (without alignments) 36.629 Million cell updates/sec

US-09-103-808-2 61 Ferfect score:

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Title:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1107863 seqs, 158726573 residues Searched:

179625 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 100%

Database

1: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
4: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
5: SIDSI/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*
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/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1994_IDAT.*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1996_IDAT.*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1996_IDAT.*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1998_IDAT.*
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/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1998_IDAT.*
/SIDS1/gogdata/geneseq/geneseqp-emb1/AA1999_IDAT.* /SIDS1/gcgdata/geneseq/geneseqg-embl/AA2001.DAT:*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS1/gcgdata/geneseg/genesegp-emb1/AA2000.DAT:* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:* A_Geneseq_19Jun03:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Human gastric canc Phage clone edl pi HIV A24 super moti HIV A24 motif env HIV A24 super moti HIV A24 super moti HIV A24 super moti HIV A01 motif env HIV A03 motif env
SUMMARIES	AAW16577 AAB6651 ABP15183 ABP14036 ABP15992 ABP15485 ABP15486 ABP19698
DB	25555555555555555555555555555555555555
% Query re Match Length DB 1	ക ക്കാര് ക്കാര്
% Query Match	0001 00004 8.0044 0.0044 0.0044 0.0044 0.0044
Score	99999999999999999999999999999999999999
Result No.	H 20 8 4 5 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

HTV All motif env	A24 motif	A24 motif	Phoe of ass	P of gas	90.00	dastri	c acid	-Src)	n pept	eptor Tvr	peptid	peptide	1. Acha	41 en		B VIII	ragment	Brain homing nepti	Immunogenic pentid	Immunogenic peptid		В	onimo	tis B v	eptide #1	tis B viru	s B viru	s B viru	is B	is	itis B	itis B	itis B	itis B	itis B
ABP22345	3	ABP24040	AAP40008	AAP40033	AAP50373	AAY51308	AAP50374	æ	\circ	AAR79712	П	AAB49571	3	AAB78533		ABJ08663	3	AAW13439	AAY46033	AAY46441	9	AAM49132	9	AAY73072	180	\vdash	ABJ06172	П	ABJ06887	99	ABJ08316	ABJ08712	879	ABJ08822	4
22	22	22	D.			_		16	21	16	21	22	14	22	23	23	15	18	20	20	20	21	21	21	22	22	23	23	23	23	23	23	23	23	23
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10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

AAW16577 standard; peptide; 9 AA. (first entry) 27-JAN-1998 AAW16577; AAW16577

RESULT 1

Human gastric cancer antigen fragment 2.

Gastric cancer, gastric cancer antigen; human leukocyte antigen; HLA; cytotoxic T lymphocyte; CTL; recombinant bacterium; recombinant virus; gastric cancer; vaccine.

Homo sapiens

EP770624-A2.

02-MAY-1997

96EP-0307163. 30-SEP-1996;

96JP-0217140. 95JP-0253491. 19-AUG-1996; 29-SEP-1995;

(AJIN) AJINOMOTO CO INC. (KIKU/) KIKUCHI K.

Suzuki M; Sato N, Sahara H, Hamuro J, Kikuchi K, Wada Y, Yasojima T;

WPI; 1997-238096/22

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                                                                                                                   This novel peptide is a fragment of a gastric cancer antigen present in a human gastric cancer cell, which when bound to a human leukocyte antigen (HLA), is capable of inducing a cytotoxic I lymphocyte (CTL) response that targets the gastric cancer cell. It is based on amino acids 1-9 of peptide 1 (AAM16576), with shows the same effect. However, peptides containing amino acids 1-8 and 1-7 of peptide 1 have no CTL inducibility, and cannot be used 17 He HLA bound peptides can be used to treat or prevent gastric cancer. Viruses, e.g. vaccinia virus, or bacteria, e.g. BCG, which contain the DNA encoding this peptide can be used as a live vaccine for preventing or treating human gastric cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel peptides that bind to immunoglobulin M antibodies and block their interaction with antigens, useful for treating rheumatoid factor biding to immunoglobulin G, autoimmune hemolytic anemia or paraneoplastic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phage display; antianaemic; cytostatic; immunosuppressive; immunoglobulin M; IgM; IgM binding; autoimmune haemolytic anaemia; paraneoplastic syndrome; multiple myeloma; cancer; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
               Gastric cancer antigen fragment present in human gastric cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                - induces cytotoxic I lymphocyte response when bound to human leukocyte antigen, for gastric cancer treatment or prevention
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 61; DB 18; Length 9; 100.0%; Pred. No. 9.3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB66551 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Page 6; 60pp; English.
                                                                                     Claim 5; Page 9; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0142389.
99US-0142389.
99US-0142524.
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                                                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-138063/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YSWMDISCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YSWMDISCW
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                           9 AA;
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                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         escape mutants. Furthermore, immunosuppressive groups that may be present
the presence of IgM in a sample and for purifying IgM from a sample. The peptides are also useful for isolating an artigen specific IgM population or for isolating an antigen bound by a specific IgM population. They are useful for treating a human disease associated with IgM antibodies such as rheumatoid factor binding to IgG, isoheamagplutinin binding to red blood cells, autoimmune haemolytic anaemia, paranecplastic syndromes, multiple myeloma or cancer. The peptides are useful for treating diseases such as cancer or an
                                                                                                                                                          autoimmune disease associated with IgM antibodies by removing IgM from serum. The peptides are capable of selectively binding to the IgM molecules of several mammalian species and to both the pentameric and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}{-}1 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                             Score 31; DB 22; Length 9;
Pred. No. 9.3e+05;
1; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV A24 super motif env peptide #63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 32; Page 180; 448pp; English.
                                                                                                                                                                                                                       monomeric forms of IgM molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP15183 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                     44.48;
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Best Local Similarity
** 4; Conserve
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                              1 YSWMDISCW
                                                                                                                                                                                                                                                                                                                                                                                                                     1 YDWIPSSAW
                                                                                                                                                                                                                                                                9 AA;
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Raker DM,
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in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPI1501 to ABP55412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human immunodeficiency virus—(IHIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABLZ5347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigen is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The result immune escape due to mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a composition (I) comprising a prepared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}{-1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vpu; vif; tat; cytotoxic T lymphocyte; CIL; immune response; epitope;
antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunodeficiency virus; env; pol; gag; nef; vpr;
                                                                                                                                                                                                                    0;
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                                                                                                                                                                     Score 30; DB 22; Length b, Pred. No. 9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Livingston BD,
                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S, Livin
Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                               ABP24036 standard; Peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kubo RT,
                                                                                                                                                                              49.2%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV A24 motif env peptide #2.
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                                                                                                                                                                                                               Conservative
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Celis E,
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                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                           3 WMDISCW 9
                                                                                                                                                                                                                                                              WFDITNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; HIV-1; human
                                                                                                                                                     8 AA;
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Baker DM,
                                                                                                                        nvention.
                                                                                                                                                                                                                                                                                                                                                                             ABP24036;
                                                                                                                                                     Sequence
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                   RESULT 4
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   555555555x8
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an group-based vaccine may be selected from conserved regions of viral or thuour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HIL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response
composition of the groups, achieving, for example, enhanced immunogentcity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPLI501 to ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          compositions comprising human immunodeficiency virus-1 (HIV-1) groups, useful for vaccinating against {\rm HIV}\text{-}1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                    Score 30; DB 22; Length 8;
Pred. No. 9.3e+05;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                1; Mismatches
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Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIV A24 super motif env peptide #172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                  ABP15292 standard; Peptide; 9 AA.
                                                                                                                                                                          49.28;
57.18;
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                                                                                                                                                                                                              4; Conservative
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Celis E,
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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| WFDITNW
                                                                                                                                    8 AA;
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                                                                                               invention
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Baker DM,
                                                                                                                                    Sequence
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Gaps

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Score 30; DB 22; Length 9; pred. No. 9.3e+05; 1; Mismatches 2; Indels

49.2%; 57.1%;

9 AA;

4; Conservative

3 WMDISCW 9

us-09-103-808-2.lim9.rag

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Best Local Similarity
               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines,
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is not possible with traditional approaches. \tt ABP11501 to \tt ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a composition (I) comprising a prepare human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be comprised.
                                                                                                                                                                                                                                                                                                                                        HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CIL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole
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                                                                                 Length 9;
                                                                                                            2; Indels
                                                                                 Score 30; DB 22;
Pred. No. 9.3e+05;
1; Mismatches 2;
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Grey HM;
                                                                                                                                                                                                                                                                                                                HIV A24 super motif env peptide #274.
                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                   ABP15394 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kubo RT,
                                                                                 49.2%;
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Celis E,
                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                 1 WFDITNW 7
                                                                                                                                      3 WMDISCW
                                                        9 AA;
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Baker DM,
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                                invention
                                                                                                                                                                                                                                                            ABP15394;
                                                         Sequence
                                                                                                            Matches
                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                      ABP15394
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escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (cTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of particularly when compared to the use of whole antigens in vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chesnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood S, Livingston BD,
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV A24 super motif env peptide #365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32; Page 186; 448pp; English.
                                                                                                                                                                                                                            ABP15485 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-0CT-2000; 2000WO-US27766
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Celis E,
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| ||: |
1 WFDITNW 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200124810-A1.
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Baker DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
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                                                                                                                                                                                                                                                                                                          ABP15485;
                                                                                                                                                  RESULT 7
ABP15485
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3 WMDISCW 9 | ||: | WFDITNW 7

Query Match

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RESULT 9
ABP19896
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CC antigens is directed largely toward variable regions of the antigen.

CC antigens is directed largely toward variable regions of the antigen.

CC tumour-associated antigens, which therefore reduces the likelihood of two tumour-associated antigens, which therefore reduces the likelihood of the whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability of combine selected groups, editeving, for example, enhanced imminorative to modify the imminorative process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) neptide arones, useful for vaccinating against \rm HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                 HIV; HIV-1; human immunodeficiency virus; env: pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Kubo RT, Grey HM;
Score 30; DB 22; Length 9;
Pred. No. 9.3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide groups, useful for vaccinating against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1.
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                                                                                                                                                                                                             ABP19698 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                               HIV A01 motif env peptide #8.
49.2%;
57.1%;
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                                                                                                                                                                                                                                                                                          (first entry)
                                      4; Conservative
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-354887/37,
                  Best Local Similarity
                                                                           3 WMDISCW 9
                                                                                                               1 WFDITNW 7
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                                                                                                                                                                                                                                               ABP19698;
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                                Matches
                                                                                                                                                                        RESULT 8
ABP19698
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0;

Gaps

· 0

Score 30; DB 22; Length 9; Pred. No. 9.3e+05; 1; Mismatches 2; Indels

49.28; 57.18;

4; Conservative

Best Local Similarity Matches 4; Conserv

Query Match

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ABP25397). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HTV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine antigens is directed largely toward variable regions of the antigen allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABPLISO1 to ABP22412 represent peptide sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
                                                                                                                                                                                                                                                              HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Pred. No. 9.3e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide groups, useful for vaccinating against HIV-1
                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 32; Page 277; 448pp; English.
ABP19896 standard; Peptide; 9 AA.
                                                                                                                                                                                                  HIV A03 motif env peptide #100.
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                                                                                                                               15-JUL-2002 (first entry)
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Celis E,
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Matches 4; Conserv
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Baker DM,
                                                               ABP19896;
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ABP24037 standard; Peptide; 9 AA.

RESULT 11 ABP24037 HIV A24 motif env peptide #3.

15-JUL-2002 (first entry)

ABP24037;

1 WFDITNW 7

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The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences selected from 51 defined amino acid sequences (ABL53347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of proup-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or
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                                                                                                                                                                                                                                                                                                                                                                                                                                  vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
antigen; vaccine; HIV infection; immunisation; virucide.
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Kubo RI, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
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                                                                       ABP22345 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                    HIV All motif env peptide #68.
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                                                                                                                                                                                                                                        (first entry)
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Celis E,
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Baker DM,
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                                                                                                                                                        ABP22345;
RESULT 10
                                          ABP22345
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ABP2597). (1) has virucide activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against {\rm HIV}\textsc{-}1
                                                                                                                                 HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic I lymphocyte; CIL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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Kubo RT, Grey HM;
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                                                                                                                                                                                                                    Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32; Page 362; 448pp; English.
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                                                                                                                                                                                                                                                                                                                                       05-0CT-2000; 2000WO-US27766.
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-354887/37
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                                                                                                                                                                                                                                                            WO200124810-A1.
                                                                                                                                                                                                                                                                                                                                                                               05-0CI-1999;
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                                                                                                                                                                                                                                                                                                    12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sette A, S
Baker DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Gaps

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Length 9;

Score 30; DB 22; Length 9; Pred. No. 9.3e+05; 1; Mismatches 2; Indels

1;

Conservative

WMDISCW 1 WFDITNW

g Qγ

Best Local Similarity
Matches 4; Conserv

Query Match

49.2%;

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The peptides of the invention are gastric secretion inhibitors used for treatment of gastro-duodenal ulcers. They are administered parenterally in doses of 1-100 mg/Kg. (Updated on 09-JAN-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                       _note= "bonded to H, a protecing gp. for the terminal amine, such as tert.-butoxy-carbonyl (Boc), benzyloxy-carbonyl (Z) or lower alkanoyl"
                                                                            Gastric secretion inhibitor; gastro-duodenal ulcer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gastric secretion inhibitor; gastro-duodenal ulcer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%; Score 29; DB 5; Length 5; 80.0%; Pred. No. 9.3e+05; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide gastric secretion inhibitors - for treating gastro-duodenal ulcers
                                                                                                                                                                                                                                                                                                                                                                                               Nisato D,
                                                     Sequence of gastric secretion inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of gastric secretion inhibitor.
                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Martinez J, Ball JP, Castro BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP40033 standard; peptide; 7 AA.
                                                                                                                                                                                                                       /label= Asp-NH2
                                                                                                                                                                                                                                                                                                                                                     (SNFI ) SANOFI SA.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 16; 17pp; French.
                                                                                                                                                                                                                                                                                                      84EP-0400787.
(updated)
(updated)
(first entry)
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(updated)
(first entry)
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Best Local Similarity
4; Conserve
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Modified-site
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                                                                                                      Jnidentified
                                                                                                                                                                                                                                                                                                                            20-APR-1983;
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            09-JAN-2003
04-FEB-1992
                                                                                                                                                                                                                                                                           07-NOV-1984.
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09-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                       Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1
                                                                             HIV: HIV-1; human immunodeficiency virus: env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CIL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
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0
                                                                                                                                                                                                                                                                                             Southwood S, Livingston BD, Chesnut R;
Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 22; Length 9; Pred. No. 9.3e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                          Grey HM;
                                                                                                                                 Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                             Claim 32; Page 362; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP40008 standard; peptide; 5 AA.
                                                      HIV A24 motif env peptide #6.
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57.1%;
                                                                                                                                                                                                                                       99US-0412863,
                                                                                                                                                                                                             05-OCT-2000; 2000WO-US27766
                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                          Sidney J,
Celis E,
                                                                                                                                                                                                                                                                 (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                 WPI; 2001-354887/37
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Best Local Similarity
Matches 4; Conserv
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1 WFDITNW 7
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                                                                                                                                                          WO200124810-A1
                                                                                                                                                                                                                                         05-OCT-1999;
                              15-JUL-2002
                                                                                                                                                                                     12-APR-2001
                                                                                                                                                                                                                                                                                          Sette A, S
Baker DM,
    ABP24040;
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Demarne

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Gaps

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Sequence

Location/Qualifiers

Key

AAP40008

RESULT 13 AAP40008

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Mon Aug

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gastric acid secretion and pancreatic exocrine promoting peptide.
                                                                                                                                                                                                                                                                                                                                             .
0
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                                                                                                                                                                                                                                                                                                                        Score 29; DB 5; Length 7; Pred. No. 9.3e+05; 0; Mismatches 1; Indels
                                                                                                                                                         Demarne H;
                                                                                                                                                                                            Polypeptide gastric secretion inhibitors – for treating gastro-duodenal ulcers
/label= benzyloxycarbonyl-Glu
                                                                                                                                                         Nisato D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gastric acid secretion; pancreatic exocrine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                         Castro BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
/label= Tyr(SO3H)
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP50373 standard; Peptide; 7 AA.
                            /label= Asp-NH2
                                                                                                                                                                                                                           Claim 6; Page 16; 17pp; French.
                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                                                                                                                                                                                                           47.5%;
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                                                                                      84EP-0400787
                                                                                                         83FR-0006492
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                                                                                                                                                                                                                                                                                                                                               4; Conservative
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                                                                                                                                                        Martinez J, Ball JP,
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                                                                                                                                                                           WPI; 1984-277632/45.
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Best Local Similarity
                                                                                                                             (SNFI ) SANOFI SA.
                                                                                                                                                                                                                                                                                                                                                                1 YSWMD 5
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                                                EP124420-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Gaps
                                                        The peptide has a glutaryl gp at the N-terminal; the C-terminal is amidated. The peptide displayed a gastric acid-promoting specific activity 6.1 fold greater than that of tetragastrin 1. See also AAP50348 (generic) and AAP50374 (specific example).
                                                                                                                                                                                                          .,
                                                                                                                                                                       Score 29; DB 6; Length 7; Pred. No. 9.38+05; 0; Mismatches 1; Indels
pancreatic exocrine-promoting activity.
                                                                                                                                                                                                                                                                                                                       4, 2003, 12:22:53
                               Example 1; Page 3; 5pp; Japanese.
                                                                                                                                                                            47.5%;
80.0%;
                                                                                                                                                                                         Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                   Search completed: August
Job time : 40 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 44, A Sequence 69, A Sequence 1480,
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Al
Sequence 9, Al
Sequence 11, 1
Sequence 15, 1
Sequence 44, p
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                                                                                                                                                                                                                                                                                                                                        Description
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Sequence 4
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                                                                                                                                                                                                                          /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/fcDCOMB.pep:*
/cgn2_6/ptcdata/1/iaa/pcTUC_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                               - protein search, using sw model
                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                    Issued_Patents_AA:*
                                                                         US-09-103-808-2
61
                                                                                                                                                                                                                                                                                                                                       DB
                                                                                          1 YSWMDISCW 9
                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                              Minimum DB seq length: 0 Maximum DB seq length: 9
                                              August
                                                                                                                                                                                                                                                                                                                              Query
Match 1
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100.0
82.0
82.0
67.2
67.2
49.2
47.5
47.5
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Perfect score:
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                                                                                                                                Searched:
                                            Run on:
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No.
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Sequence 55, Appl Sequence 64, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 62, Appl Sequence 62, Appl Sequence 62, Appl Sequence 13, Appl Sequence 134, Appl Sequence 134, Appl Sequence 134, Appl Sequence 134, Appl Sequence 111, Appl Sequence 111, Appl Sequence 111, Appl	G IMMUNE CANCER, CONTAINING THE PEPTIDE © NEUSTADT, TE 400
US-08-271-830-55 US-09-258-754-64 US-09-042-107-64 US-09-042-11-24 PCT-US95-0833-24 US-08-190-788A-18 US-08-383-44AB-23 US-08-465-391A-18 US-08-465-391A-18 US-08-465-391A-18 US-08-465-391A-18 US-08-45-62 US-08-45-62 US-08-102A-134 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-28 US-08-757-316C-38	LIGNMENTS HUMAN GASTRIC HUMAN GASTRIC HUMAN GASTRIC HUMAN GASTRIC HUMAN GASTRIC
44422.6 442.6 441.0 441.0 441.0 66933 441.0 66533 881.0 881.0 881.0 882.3 899.3 8 899.3 8 899.3 8 899.3 8 899.3 8 899.3 8 899.3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	AAHHAAAADAZZZDE OZ O 4HADOHEHHAZZZ Z Z Z Z Z
28 330 331 331 333 334 337 337 337 42 225 42 42 42 42 42 42 43 42 43 43 44 44 44 45 45 45 45 45 45 45 45 45 45	NESULT 1 US-08-723-116-2 Sequence 2, Application Patent No. 5837248 GENERAL INFORMATION: APPLICANT: KIKOCHI, APPLICANT: SATO, NO APPLICANT: SATO, NO APPLICANT: APACOIMA APPLICANT: MADA, YO APPLICANT: MADA, YO APPLICANT: MADA, YO APPLICANT: MADA, YO APPLICANT: APACOIMA APPLICANT: APACOIMA APPLICANT: APACOIMA APPLICANT: APACOIMA TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESSEE: O-BLON, ADDRESSEE: O-BLON, STATE: VA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FO MEDIUM TYPE: PLON STATE: VA COMPUTER READABLE FO MEDIUM TYPE: BACENTION STATE: APACOIMAER COMPUTER READABLE FO MEDIUM TYPE: TOBA COMPUTER READABLE FO MEDIUM TYPE: 19-AN APPLICATION NUMBER FILING DATE: 29-SI PRIOR APPLICATION DA APPLICATION NUMBER REGISTRATION NUMBER
	#D ************************************

Sequence Sequence

Sequence Sequence Sequence Sequence

Sequence

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PEPTIDE CAPABLE OF INDUCING IMMUNE RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
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  Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUDKESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
MEDIUM TYPE: Flopped disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APELICATION DATA:
APPLICATION NUMBER: US/08/723,116
FILING DATE: 30.5EP-1996
CLASSIFICATION: 530
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 253491/1995
FILING DATE: 29-SEP-1995
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 253491/1996
ATICH DATE: 19-SEP-1995
ATICH DATE: 19-SEP-1996
ATICH DATE: 19-SHG-1996
100.0%; Score 61; DB 4; 100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
                                                                                                                                                                                                                                                                             Sequence 3, Application US/08723116
Patent No. 5837248
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         YASOJIMA, TAKAHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                       SATO, NORIYUKI
SAHARA, HIROMITSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KIKUCHI, KOKICHI
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YASOJIMA, ......APPLICANT: WADA, YOSHIMASA APPLICANT: WANA, YOSHIMASU APPLICANT: SIZUKI, MANABU ....TANT: HAMURO, JUNJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.0°
Best Local Similarity 100.
Matches 8; Conservative
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                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAMURO, JUN
TITLE OF INVENTION: PI
TITLE OF INVENTION: RI
TITLE OF INVENTION: OI
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid
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                       Best Local Similarity
Matches 9; Conserv
                                                                                                         1 YSWMDISCW
                                                                                                                                                         1 YSWMDISCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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          Query Match
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                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
                                                                                                                                                                                 Query Match 100.0%; Score 61; DB 2; Length 9; Best Local Similarity 100.0%; Pred. No. 2.5e+05; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-Jun-1998
CIASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,116
FILING DATE: «UNKNOWN»
APPLICATION NUMBER: 35 217140/1996
FILING DATE: 19-AUG-1996
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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YASOJIMA, TAKAHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-103-808-2
; Sequence 2, Application US/09103808
; Patent No. 6368852
; Patent No. 6368852
; Patent No. 6368852
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TELEFAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KIKUCHI, KOKICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
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                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                          1 YSWMDISCW 9
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                                                                                                               ORGANISM:
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TITLE OF INVENTION: PERILIDE CAPABLE OF INDUCING IMMUNE
TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
CORRESPONDENCE: 4
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó:
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COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,116
FILING DATE: 30-SEP-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 25491/1995
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORBAR: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 10-821-0X
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Pred. No. 2.5e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
                                                           YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
HAMURO, JUNJI
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Patent No. 6368852
GENERAL INFORMATION:
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                                       SAHARA, HIROMITSU
KIKUCHI, KOKICHI
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HAMURO, JUNJI
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                   SATO, NORIYUKI
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Best Local Similarity 100.C
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
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                                     APPLICANT:
                                                                              APPLICANT:
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                                                                                                                      APPLICANT:
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RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADI,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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100.0%; Pred. No. 2.5e+05;
tive 0; Mismatches 0;
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APPLICATION NUMBER: 08/723,116
FILING DATE: CURNOWN>
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-821-0X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,808
FILING DATE: 24-Jun-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HUMAN
SEQUENCE DESCRIPTION: SEQ ID NO: 3;
                                                        Sequence 3, Application US/09103808
Patent No. 6368852
GENERAL INFORMATION:
APPLICANT: KIKUCHI, KOKICHI
SATO, NORIYUKI
SAHARA, HIROMITSU
YASOJIMA, TAKAHIRO
WADA, YOSHIMASA
SUZUKI, MANABU
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TELEFAX: 703-413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22202
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                   RESULT 4
US-09-103-808-3
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Score 30; DB 1; Length 7; Pred. No. 2.5e+05; 1; Mismatches 2; Indels
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APPLICANT: Breddam, Klaus
APPLICANT: Henriksen, Dennis
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: C-Terminally Amidated Peptides
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                              9663,8-US-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5580751west Center
CITY: Minneapolis
                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/039,306
FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA: US/08/431,539 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,306
                                                                                                    APPLICATION NUMBER: US/08/431,539 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08431539 Patent No. 5580751 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Nelson, Albin 1.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-530
                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 57.1
Matches 4; Conservative
                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612-332-9081
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                                                                                                                                                                                                                                                                                                                                                                                                                          7 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YSWMDIS 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YGWMDFA 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
US-08-431-539-11
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                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-431-539-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                        RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                   NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
      TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.2%; Score 41; DB 4; Length 7; 100.0%; Pred. No. 2.5e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Buchardt, ole
APPLICANT: Breaddam, Klaus
APPLICANT: Henriksen, Dennis
APPLICANT: Henriksen, Dennis
TITLE OF INVENTION: Process for the Preparation of
TITLE OF INVENTION: C-Terminally Amidated Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchant & Gould
STREET: 3100 No. 5580751west Center
                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/103,808
FILING DATE: 24-Jun-1998
CLASSIFICATION: «UNKnown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,116
FILING DATE: CURKnown>
APPLICATION NUMBER: JP 217140/1996
FILING DATE: 19-AUG-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: JP AUG-1996
ATTORNEY/AGENT INFORMATION:
ANATA: ORDER AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ); ORGANISM: HUMAN

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-103-808-4
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Patent No. 5580751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                       ZIP: 22202
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minneapolis
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US-08-431-539-9
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Gaps

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APPLICANT: Lewis C. Cantley
APPLICANT: Lewis C. Song yang
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
TITLE OF INVENTION: 77
CORRESPONDENCE ADDRESS: 77
ADDRESSE: LAHIVE & COCKFIELD
STREET: BOSTON
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/178,570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: BBI-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                     Sequence 44, Application US/08178570 Patent No. 5532167 GENERAL INFORMATION:
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> Sequence 44, Application US/08369643A

: Patent No. 6004757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Deconti, Giulio A., Jr.
REGISTRATION NUMBER: 31,503
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/17/
FILING DATE: JANUARY 7, 1994
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                   MASSACHUSETIS
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                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02109-1875
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Best Local Similarity
Matches 4; Conserv
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                 RESULT 10
US-08-178-570-44
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                                                                                                                                                                        47.5%; Score 29; DB 1; Length 6; 80.0%; Pred. No. 2.5e+05; Live 0; Mismatches 1; Indels
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80.0%; Pred. No. 2.5e+05;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Buchardt, Ole
APPLICANT: Breddam, Klaus
APPLICANT: Breddam, Klaus
APPLICANT: Henriksen, Dennis
TITLE OF INVENTION:
TITLE OF INVENTION: C-Terminally Amidated Peptides
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/431,539
FILING DATE:
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: 3100 No. 5580751west Center
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/039,306
FILING DATE: 15-ARR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/08431539
Patent No. 5580751
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Nelson, Albin J.
REGISTRATION NUMBER: 28,650
REFERENCE/DOCKET NUMBER: 966
TELECOMMUNICATION INFORMATION:
         11:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            4; Conservative
                                     LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 80.03
Matches 4; Conservative
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                                                                                                                 ; MOLECULE TYPE: peptide US-08-431-539-11
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INFORMATION FOR SEQ ID NO:
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                                                                                                TOPOLOGY: linear
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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COUNTRY:
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APPLICANT: Cantley, Lewis C.
APPLICANT: Songyang, Zhou
ITITE OF INVENTION: Substrate Specificity of Protein Kinases
FILE REFERENCE: CNS-0010F
CURRENT APPLICATION NUMBER: US/08/369,643A
CURRENT FILING DATE: 1995-01-06
EARLIER APPLICATION NUMBER: US 08/178,570
EARLIER PILING DATE: 1994-01-07
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
LENGIH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Description of Artificial Sequence:gastrin US-08-369-643-44
47.5%; Score 29; DB 1; Length 8; 80.0%; Pred. No. 2.5e+05; Live 0; Mismatches 1; Indels
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; OTHER INFORMATION: Description of Artificial Sequence: Gastrin US-08-369-643-69
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Pred. No. 2.5e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
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80.0%; Pred. No. 2.5e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: DECORTI, Gillio A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/COCKET NUMBER: BBI-004
TELECOMMUNICATION IRFORMATION:
TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 69:
                                                                                                                              MBER: US/08/178,570
JANUARY 7, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 69, Application PC/TUS9500147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 69, Application US/08369643A Patent No. 6004757
                           COMPUTER READABLE FORM:
MDIUM TYPE: Floppy disk
CMMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                             SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                                                                                                                                                              LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                               FILING DATE: JA CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YSWMD 5
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US-08-369-643-69
                                                                                                                                                                                                                                                                                                                                                                                                               US-08-178-570-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER: Pat
SOFTWARE: Pat
SEQ ID NO 69
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COUNTRY:
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Patent No. 5532167
GENERAL INFORMATION:
APPLICANT: Lewis C. Cantley
APPLICANT: Zhou Song yang
TITLE OF INVENTION: Substrate Specificity of Protein Kinases
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                                                                                                                                                                                                                                  Substrate Specificity of Protein Kinases 88
                                  1; Indels
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 Length 8;
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 Score 29; DB 3; Pred. No. 2.5e+05; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, suite 510 CITY: BOSTON
                                                                                                                                                                                                                                 TITLE OF INVENTION: Substrate Specifi
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS: AAHLYE & COCKFIELD
STREET: 60 STATE STREET, suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,570
FILING DATE: JANUARY 7, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                     Sequence 44, Application PC/TUS9500147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: DeConti, Giulio A., Jr. REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: BHI-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SED ID NO: 44:
SEQUENCE CHARACTERISTICS:
     47.5%;
80.0%;
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     Query Match 47.5
Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 amino acids
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Best Local Similarity
Matches 4; Conserv
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4 YGWMD 8
                                                                     1 YSWMD 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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                                                                                                                                                                      PCT-US95-00147-44
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US-08-178-570-69
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                                                                                                                                                        RESULT 12
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Gaps

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TITLE OF INVENTION: Substrate Specificity of Protein Kinases
NUMBER OF SEQUENCES:
ADDRESSES: 84
CORRESPONDENCE ADDRESS:
ADDRESSES: 184
CORRESPONDENCE ADDRESS:
ACTIVE: MASSACHUSETTS
ACTIVE: MASSACHUSETTS
ACTIVE: MASSACHUSETTS
ACTIVE: INANCOCCOMPARIA
SOFTWARE: ACTIVE OCCOMPARIA
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ACTIVENCE OCCOMPARIA
PRICATION NUMBER: OCCOMPARIA
PRICATION NUMBER: US 08/178,570
FILING DATE: JANUARY 1, 1944
NUMBE: DECONI, GIALIO A., Jr.
RECISENACE/CONTON NUMBER: 31,503
REPERENCE/CONTON NUMBER: 31,503
REPERENCE/CONTON
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Search completed: August 4, 2003, 12:24:33
Job time : 17 secs

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This Poge Blonk (USDIO)

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 4, 2003, 12:22:57; Search time 21 Seconds (without alignments) 50.897 Million cell updates/sec

US-09-103-808-2 61 1 YSWMDISCW 9 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

451899 seqs, 118759770 residues Searched:

46290 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:* Database :

/ cgn2_6/ptodata/2/pubpaa/USG6_NEW_PUB.ppp: / cgn2_6/ptodata/2/pubpaa/USG6_NEW_PUB.ppp: / cgn2_6/ptodata/2/pubpaa/USG7_NEW_PUB.ppp: / cgn2_6/ptodata/2/pubpaa/USG8_NEW_PUB.ppp: / cgn2_6/ptodata/2/pubpaa/USG8_NEW_PUB.ppp: / cgn2_6/ptodata/2/pubpaa/USG8_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG8_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG9_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG9_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG9_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG9_PUBCOMB.ppp: / cgn2_6/ptodata/2/pubpaa/USG9_NEW_PUB.ppp: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep;* /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep;* /cgn2_6/ptodata/2/pubpaa/US10G_PUBCOMB.pep;* /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:/ /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 134, Appl Sequence 19, Appl Sequence 10, Appl Sequence 19, Appl Sequence 19, Appl Sequence 91, Appl Sequence 94, Appl Sequence 94, Appl Sequence 97, Appl Sequence 27, Appl Sequence 27
SUMMARIES ID	US-09-847-940B-12 US-09-887-946A-12 US-09-847-946A-12 US-09-847-946A-95 US-09-847-946A-99 US-09-847-946A-99 US-09-847-946A-91 US-09-847-946A-91 US-09-847-946A-91 US-09-847-946A-91 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97 US-09-847-946A-97
DB	100 110 111 111 111 111 111
% Query Match Length DB	 00000000000000000000000000000000000
* Query Match	
Score	444444444444444444444444444444444444444
Result No.	2 4 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

Sequence 27, Appl Sequence 197, App Sequence 6, Appli Sequence 9, Appli	425 8,	Sequence 9, Appli Sequence 12, Appl Sequence 8, Appli Sequence 5, Appli	50, 51, 58,	Sequence 63, Appl Sequence 67, Appl Sequence 73, Appl Sequence 29, Appl Sequence 29, Appl	5, AF 2740 2740 5, P 5, P 174, 373,
US-10-272-3 US-10-264-3 US-10-219-8 US-09-765-6 US-09-925-7	US-09-865-018- US-09-791-378-4 US-10-165-762A	US-10-165-762A- US-09-962-298-8 US-10-304-160-5	US-09-945 US-09-945 US-09-945 US-09-945	S-09-945-24 S-09-945-24 S-09-945-24 S-09-281-49 S-09-972-65	9 US-09-863-971A-5 10 US-09-864-011A-5 11 US-09-962-298-7 11 US-09-880-748-2740 11 US-09-981-206A-5 11 US-09-981-271A-5 11 US-10-094-401-174 8 US-10-094-401-174 9 US-09-288-326-6
39.3 39.3 39.3 97.7 6	r. r. r.	6.1	36.1 7 36.1 7 36.1 7	ننننن	366.1 3366.1 3366.1 366.1 366.1 366.1 966.1 966.1
16 24 17 24 18 24 19 23 20 23		2000	o o o + 1		34/ 39 40 41 44 44 45 45 45

ALIGNMENTS

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Sequence 12, Application US/09847940B
Fatent No. US20020156000A1
GENERAL INNORMATION:
APPLICANT: May Michael J.
APPLICANT: Ghosh, Sankar
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-117CP
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US/09/847,940B
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR APPLICATION NUMBER: 2001-05-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants US-09-847-940B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
US-09-847-940B-12
                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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0; Indels 39.3%; Score 24; DB 10; 75.0%; Pred. No. 4e+05; iive 1; Mismatches 0 Query Match
Best Local Similarity 75.03
Matches 3; Conservative 1 YSWM 4 |||: 3 YSWL 6 RESULT 2 Öλ q

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Gaps

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Sequence 9, Application US/09982704; Publication No. US20020192795A1; GENERAL INFORMATION: APPLICANT: KIY, THOMAS US-09-982-704-9

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Query Match
Best Local Similarity 75.0°
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Best Local Similarity
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US-09-867-852-134
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APPLICANT: SCHULTZ, JOACHIM

TITLE OF INVENTION: CATHERSIN-L, ITS PREPRO FORM AND THE CORRESPONDING
TITLE OF INVENTION: PROPEPTIDE FROM CILIATES
TILLE OF INVENTION: DROPEPTIDE FROM CILIATES
FILE REFERENCE: 514489-3898
CURRENT APPLICATION NUMBER: US/09/982,704
CURRENT APPLICATION NUMBER: US/09/981,957
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1999-04-13
PRIOR FILING DATE: 1997-05-09
PRIOR FILING DATE: 1996-05-14
PRIOR FILING DATE: 1996-05-14
STOR APPLICATION NUMBER: 16619366.4
PRIOR FILING DATE: 1906-05-14
SOFTWARE: PALGATION NUMBER: 1206-05-14
SOFTWARE: PALGATION NUMBER: 1206-05-14
SOFTWARE: PALGATION NUMBER: 1206-05-14
SOFTWARE: PALGATION NUMBER: 1206-05-14
SOFTWARE: PALGATION VOY: 2.1
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APPLICANT: Ghosh, Sankar A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A

APPLICANT: Findeis, Mathard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
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4e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          39.3%; Score 24; DB 100.0%; Pred. No. 4e+tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Paramecium tetraurelia US-09-982-704-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.38;
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Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 39.38
Best Local Similarity 100.8
Matches 3; Conservative
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; APPLICANT: Ghosh, Sankar
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APPLICANT: Staskawicz, Brian J.
APPLICANT: Staskawicz, Brian J.
APPLICANT: Brent, Andrew F.
APPLICANT: Brent, Andrew F.
APPLICANT: Balbleck, Douglas
APPLICANT: Katagiri, Funiaki
APPLICANT: Kunkel, Barbara N.
APPLICANT: Kunkel, Barbara N.
APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
TITLE OF INVENTION: DETECTION METHODS
TITLE OF INVENTION: DETECTION METHODS
FILE REPERENCE: 00786/254002
CURRENT APPLICATION NUMBER: US/09/867,852
CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
PRIOR APPLICATION NUMBER: EARLIER PRILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1994-09-22
PRIOR PILING DATE: BARLIER FILING DATE: 1994-09-22
PRIOR PILING DATE: BARLIER FILING DATE: 1994-09-22
PRIOR PILING DATE: BARLIER FILING DATE: 1994-09-12
PRIOR PILING DATE: BARLIER FILING DATE: 1994-04-13
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE ON TIVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REPERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 95
LENGTH: 6

LENGTH: 6

LENGTH: 6

APPLICATION WINDER: 09/643,260
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 160
SEQ ID NO 95

LENGTH: 6
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US-09-847-946A-95
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42.9%; Pred. No. 4e+05;
iive 4; Mismatches 0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 134
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75.0%;
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US-09-884-767A-10

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APPLICANT: May, Michael J
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
TILE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/847,946A
FILE REPERBNCE: PEI-119
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
PRIOR PELICA DATE: 2000-08-22
SPRIOR FILING DATE: 2000-08-22
SOFTWARE: PALENTIN USE: 160
SOFTWARE: PALENTIN VET: 2.0
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US-09-847-946A-100
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APPLICANT: Ghosh, Sankar
APPLICANT: Ghosh, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.3%; Score 24; DB 11; Length 8; 75.0%; Pred. No. 4e+05;
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CURRENT FILING DATE: 2001-05-02
PRIOR PRIOR TILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
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   Application US/09847946A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Sequence 92, Application No. US200 GENERAL INFORMATION:
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APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
CURRENT: FILLIS, Gerhard
TILLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT APPLICATION NUMBER: 00/201, 261
PRIOR APPLICATION NUMBER: 60/201, 261
PRIOR FILLING DATE: 2000-05-02
PRIOR FILLING DATE: 2000-06-22
NUMBER: 09/443, 260
PRIOR FILLING DATE: 2000-06-22
NUMBER: PARCHING DATE: 2000-06-22
SOFTWARE: PARCHING TO NOW SOFTWARE: PARCHING TO SOFTWARE: PA
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US-09-847-946A-99
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Sequence 10, Application US/09884767A
Sequence 10, Application US/09884767A
Publication No. US20020192789A1
GENERAL INFORMATION:
APPLICANT: Drax Corp.
APPLICANT: Luneau, Christopher J.
APPLICANT: Ladner, Robert C
ITLE OF INVENTION: NOVEL ENTEROXINASE CLEAVAGE SEQUENCES; FILE REFERENCE: DXX-012.1 US, DYX-012.1 PCT
CURRENT APPLICATION NUMBER: US/09/884,767A
CURRENT FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 09/597,321
PRIOR FILING DATE: 2000-06-19
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: synthetic enterokinase cleavage sequence US-09-884-767A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 24; DB 10; Length 7; Pred. No. 4e+05;
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75.0%;
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Best Local Similarity 60.00
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Best Local Similarity
Matches 3; Conserv
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US-09-847-946A-92
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GENERAL INFORMATION:
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                                    US-09-847-946A-94
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US-09-847-946A-91
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APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Karbhyn
APPLICANT: Hannig, Gerbard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
CURRENT PRILING PAPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-06-22
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
APPLICANT: Pasqualini, Renata
APPLICANT: Wadih, Arap
APPLICANT: Bradesen, Dale E.
APPLICANT: Ellerby, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: DAMBER: US/09/765,086
CURRENT APPLICATION NUMBER: US/09/785,
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 9

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: synthetic peptide US-09-765-086-197
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20.09-847-946A-91
; Sequence 91, Application US/09847946A
; Publication No. US20030054999A1
                                         Sequence 197, Application US/09765086 Patent No. US20010046498A1
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75.0%;
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
LENGTH: 9
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APPLICANT: May, Michael J
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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7 SCW 9
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                       US-09-765-086-197
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RESULT: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTHER INFORMATION: Description of Artificial Sequence:NEWO binding OTHER INFORMATION: sequence US-09-847-946A-94
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APPLICANT: MAY, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findships, Kathryn
APPLICANT: Findlips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANIT-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPL-119
CURRENT APPLICATION NUMBER: US/09/847,946A
PRIOR APPLICATION DATE: 2001-05-02
PRIOR APPLICATION DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                        APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24: DB 11; Length 9;
Pred. No. 4e+05;
1; Mismatches 0; Indels
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Pred. No. 4e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/847,946A CURRENT FILING DATE: 2001-05-02 PRIOR PAPLICATION NUMBER: 60/201,261 PRIOR FILING DATE: 2000-05-02 PRIOR APPLICATION NUMBER: 09/643,260 NUMBER OF SEQ ID NOS: 160
Sequence 94, Application US/09847946A Publication No. US20030054999A1 GENERAL INFORMATION: APPLICANT: May, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/09847946A Publication No. US20030054999A1
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75.0%;
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ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 97
LENGTH: 9
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Best Local Similarity 75.03
Matches 3; Conservative
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Matches 3; Conservative
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PRIOR FILING DATE: 2000-08
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                                                                                                                           APPLICANT: Edgy, MICHAEL J
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
APPLICANT: Findeis, Mark A
ITLEANT: Hannig, Gerhard
ITTLE OF INVENITON: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
ITLE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: 05/09/847,946A
CURRENT FILING DATE: 2000-05-02
PRIOR PLICATION NUMBER: 60/201,261
PRIOR PLICATION NUMBER: 09/643,260
PRIOR PILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // FEATURE:
// OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
// OTHER INFORMATION: sequence
US-09-847-946A-98
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US-10-272-411-27
Sequence 27, Application US/10272411
Publication No. US20030100068A1
GENERAL INFORMATION:
APPLICANT: Barnes Jowish Hospital
APPLICANT: Lam, Jonathan
APPLICANT: Teitelbaum, Steven
TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
FILE REFRENCE: 60019620-0202
CURRENT APPLICATION NUMBER: US/10/272,411
PRIOR FILING DATE: 2001-10-15
PRIOR FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 52
SOFTWARRE: PatentIn Version 3.1
                                       Sequence 98, Application US/09847946A Publication No. US20030054999Al GENERAL INFORMATION:
APPLICANT: May, Michael J APPLICANT: Ghosh, Sankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.3
Best Local Similarity 75.0
Matches 3; Conservative
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; ORGANISM: Homo sapienS
US-10-272-411-27
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4 YSWL 7
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RESULT 14
US-09-847-946A-98
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Search completed: August 4, 2003, 12:25:00 Job time: 21 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

(without alignments) 57.701 Million cell updates/sec August 4, 2003, 12:21:46; Search time 15 Seconds

US-09-103-808-2 61 1 YSWMDISCW 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

789

Minimum DB seq length: 0 Maximum DB seq length: 9

Listing first 45 summaries Post-processing: Minimum Match 08 Maximum Match 1008

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	neutromodulatora	neuromodulatory pe	~ :	neuronentide Crb-A			cholecystokinin -	cholecvstokinin -	leucokinin VIII -	phyllocaerulein -	locustamyoinbibiti	nev-kinin 2 - nena	neuropentide Grb-A			2			reger fage		truntonbullin had	٦,	20140	receptor	rondana r	⊂	٠,	9 1	leucokinin V - Mad
SOMMAKIES	A	S33244	S33245	S33246	C57444	PT0272	A32516	PQ0012	A43001	JS0318	A61357	AKLQIM	PD0028	A57444	B57444	B34835	PT0270	A31263	B35640	C61512	JS0316	A61081	T13818	PT0661	PT0580	A61068	PN0649	510596	D61512	JS0315
	Length DB	7 2	7 2					8 2														7 2								
* Query	Match Ler	44.3	٠	⊣	7.	37.7	36.1	36.1	36.1	36.1	•	5						27.9					26.2		4			24.6	24.6	24.6
	Score	27	27	25	23	23	22	22	22	22	$^{\circ}$	21.5	21	20	19	18	18	17	17	17	17	16	16	15	15	15	15	15	15	15
Result	No.	1	5	m	4	ഗ	۱۹	_	no o	, עב) T	1	12	13	14	15	16	17	18	13	20	21	22	23	24	25	26		28	29

leucokinin VII - M T-cell receptor ga adipokinetic hormo neuropeptide Grb-A IG Heavy chain CRD gene c-mpl protein dihydrofolate redu T-cell receptor be triacylglycerol li IGH chain V-D-J r T-cell receptor be probable H-transp virotoxin - destro angiotensin-conver leucine-tRNA ligas growth hormone rec
JS0317 A38887 A54244 D57444 P10299 158350 B31263 P10519 S57274 PH1602 P10519 A58725 A58725 A58725 A58725 A58725 A66023
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ALIGNMENTS

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24-5 K. Solat	;0
533244 neuromodulatory peptide WWamide-1 - giant African snail c;Species: Achatina fulica (giant African snail) c;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997 C;Accession: S33244 EEBS Lett. 323, 104-108, 1993 A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia (A;Reference number: S33244; MUID:93265912; PMID:8495720 A;Reference number: A;Reference number: S33244; MUID:93265912; PMID:8495720 A;Reference number: A;Reference number: A;Reference number: S33244; MUID:93265912; PMID:8495720 A;Reference number: A;Reference number: A;Reference number: S33244; MUID:93265912; PMID:8495720 A;Reference number: A;Reference number: A;Reference number: A;Reference number: S33244; MUID:93265912; PMID:8495720	Query Match 44.3%; Score 27; DB 2; Length 7; Best Local Similarity 42.9%; Pred. No. 2.8e+05; Matches 3; Conservative 2; Mismatches 2; Indels 3 WMDISCW 9 :: 1 WKEMSVW 7
533244 neuromodulatory peptide Wwam C;Species: Achatina fulica (C;Date: 19-Mar-1997 #sequenc C;Accession: S33244 R;Minakata, H; Reda, T; M FEBS Lett. 323, 104-108, 199 A;Title: Wwamide-1, -2 and -A;Reference number: S3244; A;Accession: S33244 A;Status: preliminary A;Molecule type: protein A;Residues: 1-7 <min></min>	atch 44.3 cal Similarity 42.9 3; Conservative 3 WMDISCW 9 1:1 1 1 WKEMSVW 7
s33244 neuromodu C; Species C; Date: 1 C; Accessi R; Minakat FEBS Lettle: A; Title: A; Referer A; Actus: A; Molecul A; Residue	Query Match Best Local Matches Qy

RESULT 2 S33245

C. Species: Achatina fulica (giant African snail)
C. Species: Achatina fulica (giant African snail)
C. Date: 19-Mar-1997 *sequence_revision 19-Mar-1997 *text_change 24-Jul-1997
C. Accession: 333245
R. Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WMamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia contents of the con

A, Accession: 33245 A, Status: preliminary A, Molecule type: protein A; Residues: 1-7 <MIN>

0; Score 27; DB 2; Length 7; Pred. No. 2.8e+05; 2; Mismatches 2; Indels Query.Match
Best Local Similarity 42.9%;
Matches 3; Conservative

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Gaps

3 WMDISCW 9 | ::| | | WREMSVW 7 δ qq

RESULT 3

S33246 neuromodulatory peptide WWamide-3 - giant African snail C;Species: Achatina fulica (giant African snail)

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Gaps

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C; Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 C; Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000 C; Accession: A32516 R; Shively, J; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J. Am. J. Physiol. 252, 6272-6275, 1987 Apritle: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in A; Reference number: A32516; MUID:87153871; PMID:3826354
                                                                                                                                                                                                                                                                                  A,Molecule type: protein
A,Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NyAlternate names: CCK
NyAlternate names: CCK
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C;Accession: P00012
R;Fan, Z.W.; Eng, J., 1984
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: P00012; MUID:88234141; PMID:3375140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.1%; Score 22; DB 2; Lk
100.0%; Pred. No. 2.8e+05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.1%; Stor.
100.0%; Pred. No. 2.
... 0; Mismatches
          C; Species: Canis lupus familiaris (dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cholecystokinin - southeastern quoll
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
B;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: C57444
A;Accession: C57444
A;Accession: C57444
A;Accession: C57444
A;Accession: C57444
A;Residues: 1-9 <LOR>
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C'Species: Homo sapiens
C'Accession: PT0272
R'Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
R'Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
A'Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; MUID:91108337; PMID:1899102
                                                                             R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of
A;Reference number: S33244; MUID:93265912; PMID:8495720
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C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33246
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Pred. No. 2.8e+05;
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Pred. No. 2.8e+05;
2; Mismatches 1;
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A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
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50.0%;
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                                                                                                                                                                                                                             A; Accession: S33246
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-7 <MIN>
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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Matches 3; Conser
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Per Kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C;Accession: PD0028
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devrec Blochem: Biophys. Res. Commun. 248, 406-411, 1998
A;Title: Identification of one tachykinin- and two kinin-related peptides in the brai A;Reference number: PD0027; MUID:98342103; PMID:9675150
                                                         spontaneous contractions of the hindgut a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuropeptide Grb-AST B2 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: B5744
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
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                         A; Residues: 1-9 < SCH>
C; Comment: This peptide hormone suppresses spontaneous contractions C; Superfamily: locustamyoinhibiting peptide
C; Keywords: amidated carboxyl end; hormone
F; 9/Modified site: amidated carboxyl end (Trp) **status experimental
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A; Residues: 1-6 <NIE>
C; Comment: This peptide belongs to myotropic neuropeptides.
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                                                                                                                                                 Score 21.5; DB 1;
Pred. No. 2.8e+05;
3; Mismatches 2;
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Pred. No. 2.8e+05;
0; Mismatches 2;
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40.0%; Pred. No. 2.8e+05;
.ive 2; Mismatches 1;
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60.0%;
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ilarity 33.3%;
Conservative
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Best Local Similarity 60.03
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
         A; Molecule type: prote
A: Residues: 1-9 <SCH>
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A/Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona A; Reference number: A61357; MUID:70005484; PMID:5824931
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A.Residues: 1-9 <ANA>
A.Residues: 1-9 <ANA>
S.Superfamily: qastrin
C.Reywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Reinding site: sulfate (Tyr) (covalent) #status experimental
F:9/Modified site: amidated carboxyl end (Phe) #status experimental
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                                                                                                                                                                                           cockroach)
07-Sep-1990 #text_change 20-Jun-2000
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C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61357
         Gaps
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A.Moleucle type: protein
A.Residues: 1-8 -4HDL.
C.Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate
C.Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) *status experimental
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R; Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A; Title: Isolation, primary structure and synthesis of leucokinins VII
A; Reference number: JS0317
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         Indels
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Pred. No. 2.8e+05;
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100.0%; Pred. No. ...
0; Mismatches
   Mismatches
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C;Species: Leucophaea maderae (Madeira
C;Date: 07-Sep-1990 #sequence_revision
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Matches 3; Conservative
3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Matches
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29.5%; Score 18; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels
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Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: B57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 4, 2003, 12:21:01; Search time 11 Seconds (without alignments) 38.476 Million cell updates/sec Run on:

US-09-103-808-2 61 1 YSWMDISCW 9 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

251 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES		WWA1 ACHEU	WWA3 ACHFU		PTSP BOMMO				LMIP_LOCMI	LCK4_LEUMA	LCK6_LEUMA	EIUI_LITRU		LOK1_LOCMI	AKH_LIBAU	LCK1_LEUMA	LCK2_LEUMA	LCK3_LEUMA	LCK5_LEUMA	LCK7_LEUMA	ACI_THUAL	TPFY_PACDA	AL16_CARMA	D1_NEPNO	OXYT_BUFRE	ALL4_CARMA		BRHP_CONIM	ALIS_CARMA	ALL /_CARMA	- 1		ALL4_CALVO	ALL4_CYDPO	HTF1_PERAM
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12 19.7 8 HTF2_PERAM P04549 periplaneta 12 19.7 8 HTF_TENMO P825419 tenebrio mo P82929 bos taurus 12 19.7 9 1 RE42_LITRU P82929 bos taurus P82929 bos taurus 12 19.7 9 1 TALL_PICJA P17441 pichia jadi P1745 P17441 pichia jadi P18.0 9 1 TALL_PICJA P17441 pichia jadi P18.0 7 1 TYLL_LITRU P82065 Litoria rub P80709 Carcinus ma P18.0 8 1 AKHG_GRYBH P80709 Carcinus ma P18.0 8 1 AKHG_GRYBH P825423 melolontha 11 18.0 8 1 AKH_TABAT P14595 tabanus atr	MALLACHEU WARLACHEU WARLACHEU WARLACHEU E 755919; I 01-JUN-1994 (Rel. 29, Created) I 01-JUN-1994 (Rel. 29, Last sequence update) I 01-JUN-1994 (Rel. 29, Last sequence update) I 01-JUN-1994 (Rel. 29, Last annotation update) E Warmide-1. S Achatina fulica (diant African snail). E Warmide-1. S Achatina fulica (diant African snail). S Achatina fulica (diant African snail). S Achatina fulica (diant African snail). S EQUENCE. SIGNILIAE-93265912; PubMed-8495720; MINIAE-Ganglion; MEDLINE-93265912; PubMed-8495720; MINIATIS And 13: Novel neuromodulatory peptides isolated from SERGEL 3: novel neuromodulatory peptides isolated from Ganglia of the African giant snail, Achatina fulica."; FEBS Lett. 323:104-108(1993). -1 SYSTEM. INNIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS SYSTEM. INNIBITS ACTIVITY ON A CENTRAL NEURON. NOUS REST And 100 (1993). -1 STATEM. 100 (1993). -1 STATEM. 100 (1993). -1 AMIDATION. SEQUENCE 7 AA: 993 WW: 7362D5869B041310 CRC64; OUGLY MATCH A 42.9%; Pred. No. 1.38+05; Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 1: 1.1 1 WREMSVW 7	JLT 2 "ACHFU WWAS ACHFU STANDARD; PRT; 7 AA. #935921; 01-UUN-1994 (Rel. 29, Created) 01-UUN-1994 (Rel. 29, Last sequence update) 01-UUN-1994 (Rel. 30, Last annotation update) 01-UUN-1994 (Rel. 30, Last annotation update) 01-SURJANDARD; PRT; Sequence update) 01-SURJANDARD; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora; Sigmurethra; Achatinoidea; Achatinidae; Achatina. Comparison of the comparison of the Mark of the Achatina of the Arrican giant shall, Nomoto K.; Winakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; Wanakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.; Wanakata H., Ikeda T., Muneoka Y., Robayashi M., Nomoto K.; Wananide-1., 2 and -3: novel neuromodulatory peptides isolated from FEBS Lett. 323:104-108(1993).
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	RESULT 1 WWALLACHEU TO WWALLACHEU TO 01-0UN-10 DT 01-0UN-10 DE WWANTGE-OS ACATIONS OC SIGNUCET OC SYST OC STATE OCH MATCH DEST LOCAL MATCH BEST LOCAL MATCH DEST LOCAL	RESULT 2 WWA3_ACHFU ID WWA3_A AC P3592 DT 01-001 DT 01-001 DE Wannic OS Achati OC SURATY OC SURATY OC NOBL-IN RN (1]-INSUE RX MEDLIN RA MINAKA RT GWANI

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Leucophaea maderae (Madeira cockroach)
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                                                                                                                                                                                    40.28;
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                                                                                                                                              SEQUENCE 9 AA; 1090 MW;
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Best Local Similarity 44...
Gest Local 4; Conservative
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P19990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Stylommatophora,
Sigmurethra, Achatinoidea, Achatinidae, Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minakata H., Ikeda T., Muneeka Y., Kobayashi M., Nomoto K.; "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snall, Achatina fulica."; PEBS Lett. 323:104-108(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41.0%; Score 25; DB 1; Length 7; 42.9%; Pred. No. 1.3e+05; tive 1; Mismatches 3; Indels
                                                                                           Score 27; DB 1; Length 7; Pred. No. 1.3e+05; Alsmatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 7 AMIDATION.
7 AA; 964 MW; 7362D5B686D32310 CRC64;
                                       AMIDATION.
7362D5B69B132310 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bombyx mori (Silk moth).
                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA.
                                                                                                                                                                                                                                                                                                           7 AA.
                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Achatina fulica (Giant African snail).
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J. Biol. Chem. 274:31169-31173(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Ganglion;
MEDLINE=93265912; PubMed=8495720;
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                                                                                             44.3%;
ilarity 42.9%;
Conservative
                                                       7 AA; 965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Conservative
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MOD_RES 7 7 7
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               Neuropeptide; Amidation.
MOD_RES 7 7 7 SEQUENCE 7 AA; 965 MW
                                                                               Query Match
Best Local Similarity
3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombycidae; Bombyx.
NCBI_TaxID=7091;
     PIR; S33244; S33244.
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Best Local Similarity
Matches 3; Conserv
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P82003;
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                                                                                                                                                                                                                                                                                                         WWA2_ACHFU P35920;
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PTSP_BOMMO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THE NEEDEN HORMONE INDUCES GALL BLADDER CONTRACTION AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION IN THE BRAIN IS NOT CLEAR.

-1- STMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

PIR; A43001; A43001.

PIR; PQ0012: PQ002.

PROSITE; PS00259; GASTRIN; 1.
                                                                                                                                                                                                                                                                           Gaps
Kataoka H.;
J. Biol. Chem. 275:9892-9892(2000).
-!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dasyurus viverrinus (Southeastern quoil).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontla; Macropodidae; Macropus.
NCBI_PaxID=9315, 9279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                            Length 9;
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                                                                                                                                                                                                                                                                           2; Indels
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                                                                                                                                                          AMIDATION.
3878C5B4472AB6C3 CRC64;
                                                                                                                                                                                                                          Score 24.5; DB 1;
Pred. No. 1.3e+05;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VIII (L-VIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-SEP-2003 (Rel. 42, Last annotation update)
Cholecystokinin (CCK).
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100.0%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA.
                                                                  gland.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR
Hormone; Amidation.
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AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macropus eugenii (Tammar wallaby), and
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TISSUE=Brain;
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Cephalomyotropins."
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Best Local Similarity
2; Conserve
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Best Local Similarity
Matches 2; Conserv
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5 HSW 7
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                                                                                                     TISSUE=Head;
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                                                                                                                                                                                                        SEQUENCE
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MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regul. Pept. 36:111-119(1991).
-1- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -:- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBOESOPHAGEAL GANGLION.
                                                            MEDLINE-92179466; PubMed-1796179; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; "Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria.";
                                                                                                                                                                                                             0;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
                                                                                                                                                                                                                                                                                                                                                                       Caelifera; Acridomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21.5; DB 1; Length 9; Pred. No. 1.3e+05;
                                                                                                                                                                                       36.1%; Score 22; DB 1; Length 8; 100.0%; Pred. No. 1.3e+05; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels

        MOD_RES
        8
        AMIDATION.

        SEQUENCE
        8 AA; 902 MW; 736365AB59CAADD8 CRC64;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387D7DD4472AB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Last Sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Locustamyoinhibiting peptide (LOM-MIP).
Locusta migratoria (Migratory locust).
                                                                                                                                                                                                                                                                                                                                                                   Neoptera; Orthopteroidea; Orthoptera; Caeliff
Acridoidea; Acrididae; Oedipodinae; Locusta.
                                                                                                                                                                                                                                                                                              9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                              (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1991 (Rel. 18, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 9
9 AA; 1060 MW;
                                                                                                                                                                                                          3; Conservative
                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A60065; AKLQIM.
Amidation; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Conservative
                  Blaberidae; Leucophaea.
NCBI_TaxID=6988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 SWMDISC-W 9
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                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AWQDLNAGW
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=7004;
                                                                                                                                                                                                                                      111
5 YSW 7
                                                                                                                                                                                                                            1 YSW 3
                                                       rissur=Head:
                                                                                                                                                                                                                                                                                                                    01-JUL-1993
01-OCT-1993
                                                                                                                                                                                                                                                                                                             01-JUL-1993
                                                                                                                                                                                                                                                                                         LMIP_LOCMI
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                                               SEQUENCE.
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ID LCK4_LI
AC P21143;
DT 01-MAY
                                                                                                                                                                                                                                                                       RESULT 7
LMIP_LOCMI
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                                                                                                                                                                                                                                                                                                                                                          STIMULATES CONTRACTILE
                                                                                                                                                                                                                                      Holman G.M., Cook B.J., Nachman R.J.; "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of
                                                                                     Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Leucokinin VI (L-VI)
Leucophaea maderae (Madeira cockroach)
Eukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Neoptera, Orthopteroidas, Dictyopterae, Slattaria; Blaberoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17; DB 1; Length 8;
Pred. No. 1.3e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 17; DB 1; Length 8; 66.7%; Pred. No. 1.3e+05; live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         8 8 AMIDATION.
8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 8 A3; 935 MW; 9D6365BlE9D5A5A6 CRC64;
                                                                                                                                                                                                                                                                                                                        Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE ST.
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
Neuropeptide; Amidation.
MOD_RES 8
AMIDATION
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokinin IV (L-IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
                                                               Leucophaea maderae (Madeira cockroach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=87052651; PubMed=2877794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Conservative
                                                                                                                                                                                                SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                Blaberidae; Leucophaea.
NCBI_TaxID=6988;
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PIR; A61068; A61068.
Neuropeptide; Amidation.
MOD_RES 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                            SEQUENCE.
TISSUE=Corpora cardiaca;
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=6966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SW 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                              LOK1_LOCMI P41491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dragonfly.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ΩŽ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Iwakoshi E., Hisada M., Minakata H.; "Cardioactive peptides isolated from the brain of a Japanese octopus, Octopus minor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Octopus minor (Octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
                                                                                                                                                                                             Wabnitz P.A., Bowle J.H., Tyler M.J., Wallace J.C.; "Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria
                                                                                     Litoria rubella (Desert tree frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
Pelodryadinae; Litoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Cardioactive, has both positive chronotropic and inotropic effects on the heart, Ocp-4 is a 1000 time less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                         26.2%; Score 16; DB 1; Length 6; 100.0%; Pred. No. 1.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 2 D-SERINE (IN OCP-4).
4 AA; 463 MW; 6AB365B810000000 CRC64;
                                                                                                                                                                                                                                                                                                                 6 AA; 792 MW; 6683704772C9A000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%; Score 15; DB 1; Le 100.0%; Pred. No. 1.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBGELLULAR LOCATION: Secreted.
-!- PTM: Ocp-4 has D-Ser instead of L-Ser.
-!- MASS SPECTROMETRY: MW-395.2; METHOD-MALDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) cardioactive peptides Ocp-3/Ocp-4.
                                 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AA.
         6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                      AMIDATION.
                                                                                                                                                                                                                                                   Aust. J. Chem. 52:639-645(1999).
-- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Skin.
Amphibian defense peptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20336815; PubMed=10876044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides 21:623-630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                         2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                active than Ocp-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormone; D-amino acid.
                                                                                                                                                                                     TISSUE-Skin secretion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                             NCBI_TaxID=104895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=89766;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SW
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                                                                                                                                                                                                                                                                                                                                                                                                                   2 MM
         EI01_LITRU
P82096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OCP3_OCTMI
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                                                                            Electrin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE,
                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                         SEQUENCE.
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                         rubella.
                                                                                                                                                                                                                                                                                                         MOD RES
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OCP3_OCTMI
EI01_LITRU
                                                                                                                                                                                                                                                                                                                                                                           Matches
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de Loof A.;
"Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolation, primary structure and synthesis.";
Regul. Pept. 37:49-57(1992).
-; FUNCTION: Myotropic peptide. May be important in the stimulation
of ion transport and inhibition of diuretic activity in Malpighian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR, S10596, S10596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The putative ancestral peptide of the adipokinetic/red-pigment-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANOSITE; PS00256; AKH; 1.
Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MX-1992 (Rel. 22, Created)
01-REB-1994 (Rel. 28, Last sequence update)
01-REB-1903 (Rel. 141, Last annotation update)
Adipokinetic hormone (AKH).
Libellula aurripennis (Skimmer dragonfly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
                                                                                                                                                               Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92262851; PubMed-1585017;
Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  concentrating hormone family isolated and sequenced from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.6%; Score 15; DB 1; Length 6; 100.0%; Pred. No. 1.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 6 AMIDATION.
6 AA; 654 MW; 686365A5B9CDB000 CRC64;
                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nfly.";
Chem. Hoppe-Seyler 371:475-483(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
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Search completed: August 4, 2003, 12:23:10 Job time : 11 secs
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                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Comp. Biochem. Physiol. 84C:205-211(1986).
-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                           TISSUE-Head;
Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
                                                        ;
                                                                                                                                                                                                                                     Leucophaea maderae (Madeira cockroach).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Orthopteroidea, Dictyoptera, Blattaria, Blaberoidea,
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 18, Last annotation update)
Leucokhinin II (L-II),
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Blaberidae;
Blaberidae; Leucophaea.
                                                     Indels
                       24.6%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 1.38+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.6%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 1.3e+05; tive 0; Mismatches 0; Indels
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978 MW; 8665A771A9C452D6 CRC64;
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8 AA; 893 MW; DC6365B449CDC76A CRC64;
                                                                                                                                                                                   01-MAY_1991 (Rel. 18, Created)
01-MAY_1991 (Rel. 18, Last sequence update)
01-MAY_1991 (Rel. 18, Last annotation update)
Leucokinin I (L-I).
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Best Local Similarity 100.
Matches 2; Conservative
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NCBI_TaxID=6988;
          8 AA;
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P21140;
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P21141;
 SEQUENCE
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                                   24.6%; Score 15; DB 1; Length 8; 100.0%; Pred. No. 1.3e+05; live 0; Mismatches 0; Indels
  AMIDATION.
DC6365A5B9C8676A CRC64;
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852 MW;
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8 AA;
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OM protein - protein search, using sw model

Run on:

August 4, 2003, 12:21:21; Search time 32 Seconds (without alignments) 72.577 Million cell updates/sec

US-09-103-808-2 61 Perfect score:

1 YSWMDISCW 9 Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters: 830525 seqs, 258052604 residues

775

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_23:* Database

sp_fung:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_unclassified:* sp_virus:*
sp_vertebrate:* sp_rvirus:*
sp_bacteriap:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_plant:*
sp_rodent:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

035835 rattus sp. 015888 home sapien 09try3 sus sp. ins 09t4y2 asterina pe 089131 borrelia bu 090126 borrelia bu 016386 home sapien 09y4x6 home sapien 094xe6 tectocoris 049223 glycine max 015890 homo sapien Q9et18 mus spretus Q9et17 mus caroli Q9et16 mesocricetu Description SUMMARIES Q8GL31 Q8GL26 Q16386 Q9Y4X6 Q9ET18 Q9ET17 Q9ET16 049223 Q15890 035835 Q15888 Q9TRY3 Q9T4Y2 Query Match Length DB Score 20 20 119 117 117 Result . ⊵

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ALIGNMENTS

Rattus sp. Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. Gaps TISSUE-Testis,
MEDLINE-98008057; PubMed=9581555;
HOSPITAL V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
HUMAN and rat testis express two mRNA species encoding varients of NRO convertase, a metalloendopeptidase of the insulinase family.";
Biochem. J. 327:773-779(1997).
EMBL; X93208; CAA63695.1; -.
SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64; ; 34.4%; Score 21; DB 11; Length 8; 66.7%; Pred. No. 8.3e+05; 0; Indels Last sequence update) Last annotation update) 8 AA. 8 AA. 1; Mismatches Created) 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19, Query Match
Best Local Similarity 66.79
Matches 2, Conservative PRELIMINARY; PRELIMINARY; SEQUENCE FROM N.A. NCBI_TaxID=10118; :|| 6 TCW 8 7 SCW 9 ORF1 protein. Q15888 Q15888; 01-NOV-1996 (01-NOV-1996 (01-DEC-2001 (035835; 035835 RESULT 1 035835 C1 RESULT 015888 δ a PP PP PP

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(TrEMBLrel. 01, Created) (TrEMBLrel. 01, Last sequence update) (TrEMBLrel. 19, Last annotation update)

050832 methanococc 094vc6 varanus pil

Q50832 Q94VC6

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                                                                          Mitochondrion.
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SEQUENCE
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Q8GL26;
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Shimmasaki S., Gao L., Shimonaka M., Ling N.;
"Isolation and molecular cloning of insulin-like growth factor-binding
protein-6.";
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                                                                                     Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
(Clone XP15H8A) (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                               Caskey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL; Li32069; AAA71878.1; -.
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Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
NCBI_TaxID=7594;
                                                                                                                                                                                                               32.8%; Score 20; DB 4; Length 8; 100.0%; Pred. No. 8.3e+05; Live 0; Mismatches 0; Indels
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01-MAX-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                           0315A37EAB5B0763 CRC64;
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Asterina pectinifera (Starfish).
Mitochondrion.
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8 AA; 1068 MW;
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Best Local Similarity 100.
Matches 2; Conservative
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SEQUENCE FROM N.A.
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                                                                               TISSUE=Placenta;
                                               NCBI_TaxID=9606;
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Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Sh-2-82;
Stevenson B., Miller J.C.;
"Comparative analyses of Borrelia burgdorferi erp genes and their cp32
prophages: conservation amidst diversity.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142089; AAN17869.1; -.
[1]
SEQUENCE FROM N.A.
MEDLINE-89334669; PubMed=2766382;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
Jacobs H.T., Asakawa S., Araki T., Miura M.J., Watanabe K.;
Jacobs H.T., Asakawa M.J., Watanabe H.J., Wa
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Plasmid group cp32-5.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TaxID=139;
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Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
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Last annotation update)
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50.0%;
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9 AA; 1206 MW;
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2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.1
Best Local Similarity 50.0
Matches 3; Conservative
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PRT;
                                 27.9%;
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60.0%;
                                                                                                                                                                                                              Neuropeptide Y (Fragment).
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 60.0
nes 3; Conservative
                                                                                                                                                        PRELIMINARY;
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Matches 3; Conservative
                  Ouery Match
Best Local Similarity
2; Conserve
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                                                                           4 MDISC 8
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Q9ET18;
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Matches
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EMBL: AJ243097; CAB45408.1; -... 8 8 8 SEQUENCE 8 AA: 767 MW; EE6EBDDEB862D5B6 CRC64:
                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                DEQUENCE FROM N.A.

MEDLINE=95400293; PubMed=7670464;
Budarf M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C.,
Sellinger B., Michadd D., Driscoll D.A., Emanuel B.S.;
"Cloning a balanced translocation associated with DiGeorge syndrome and identification of a disrupted candidate gene.";
Nat. Genet. 10:269-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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0
                                                                   Score 19; DB 2; Length 9;
Pred. No. 8.3e+05;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY142092; AAN17873.1; -.
Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.3e+05;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 19; DB 4; Length 9;
                                                       5A4A244330504373 CRC64;
                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 9 AA; 1137 MW; 734911A69446837B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                       9 AA.
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                                                                                                   1; Mismatches
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(TrEMBLrel. 12, Last seq
(TrEMBLrel. 19, Last anno
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40.0%;
                                                                              31.1%;
50.0%;
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9 AA; 1206 MW;
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EMBL; S79485; AAD14301.1; -.
NON_TER 1 1
                                                                                                 2; Conservative
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                              Homo sapiens (Human).
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                                                                                       Best Local Similarity
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1 YKWI 4
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01-NOV-1999 (
01-DEC-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRET/E1;
Iaylor B.A., Whek C., Phillips S.J.;
Multiple obesity OTLs identified in an intercross between the NZO (New Zealand obese) and the SM (small) mouse strains.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF286200; AAG01474.1;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor B.A., Whek C., Phillips S.J.;
"Multiple obesity OTLS identified in an intercross between the NZO (New Zeland obese) and the SM (small) mouse strains.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF286201; AAG01475.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide Y (Fragment).

Mus caroli (Wild mouse) (Ricefield mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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        Length 8;
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                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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SEQUENCE 8 AA: 1033 MW; 297685A76AAB1734 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Score 17; DB 4; Le
Pred. No. 8.3e+05;
L; Mismatches 2;
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Pred. No. 8.3e+05;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                         AA.
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Glycine max (Soybean).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Glycine.
                                                                                                                                                                                     Laux T., Goldberg R.B.; "A plant DNA binding protein shares highly conserved sequence motifs with HMG-box proteins."; with HMG-box proteins."; Nucleic Acids Res. 19:4769-4769(1991).
                                                                                                                                                                                                                                                                                                                                                                          26.2%; Score 16; DB 10; Length 7; 40.0%; Pred. No. 8.3e+05; tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
SIRAIN-CV. BSSEX; TISSUE-ROOT;
MARAILINGAM R., Knap H.T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF047050; AAC03556.1; -.
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               SEQUENCE 7 AA; 850 MW; 6AAAABB378637810 CRC64;
                                                                                                                                                              STRAIN-cv. Essex; TISSUE-Root;
MEDLINE-91367679; PubMed-1891369;
                                                HMG-1-like protein (Fragment).
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nes 2; Conserv
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MAGL. Biol. Bvol. 18:1828-1832(2001).

Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                             SEQUENCE FROM N.A.

Taylor B.A., Whek C., Phillips S.J.;

Taylor B.A., Whek C., Identified in an intercross between the NZO Multiple obesity QTLS identified in an intercross between the NZO NWW Zealand obese) and the SM (small) mouse strains.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF286202; AAG01476.1; -.
                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
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                                                                                                                                                                                                                                                                                                                                           Length 8;
                                                                                                                                                                                                                                                                                                                                         27.9%; Score 17; DB 11; Length 8; 60.0%; Pred. No. 8.3e+05; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytochrome c oxidase subunit III (Fragment).
                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Neuropeptide Y (Fragment).
Mesooricetus auratus (Golden hamster).
                                                                                                                                                                                                                                                                                                               8 AA; 1033 MW; 297685A76AAB1734 CRC64;
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                                          PRT;
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nes 3; Conservative
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                                                                                                                                                                                  NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                      5 DISCW 9
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SEQUENCE
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                                        Q9ET16
Q9ET16;
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049223
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Matches
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Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
                                                                                                Colone XP19612A) (Fragment).

Homosopiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
                                                                                                                                                                                                                          ....., Chinault C.A., Bailey J., Couch L., Xiong M.
.askey C.T.H.;
"Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries.";
Hum. Mol. Genet. 0:0-0(1995).
EMBL; L32083; AAA;3880.1; -.
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                                                               01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.2%; Score 16; DB 4; I
llarity 66.7%; Pred. No. 8.3e+05;
Conservative 1; Mismatches 0;
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AA.
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                       Q15890;
01-NOV-1996 (TrEMBLrel. 01, Created)
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PRT;
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AC Q50832;
DT Ol-NOV-1996 (TrEMBLrel. 01, Created)
DT Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT Ol-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT Ol-NOV-1996 (TrEMBLrel. 01, Last annotation update)
OS Methanococcus voltae.
OC Archaea; Buryarchaecta; Methanococci; Methanococcales;
OC Methanococcaee; Methanococcus.
OC Methanococcaee; Methanococcus.
OC Methanococcaee; Methanococcus.
OX NOBL_TaxID=2188;
RN (1)
RN SEQUENCE FROM N.A.
RX MEDLINE-85230552; PubMed=4006907;
RA MEDLINE-85230552; PubMed=4006907;
RN Methanococcus voltae DNA.";
RN Methanococcus
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